

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 9, 2001, 09:00:33 ; Search time 258.85 Seconds
(without alignments)
9826.865 Million cell updates/sec

Title: US-09-694-777-14
Perfect score: 2967
Sequence: 1 atgacacgtgctgggggacg.....gagacatttgagagccacg 2967

Scoring table: IDENTITY-NUC
Gap 10.0, Gapext 1.0

Searched: 930621 seqs, 428662619 residues
Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: N_Geneseq_1101.*
2: /SID88/gcgcdata/geneseq/geneseqn/NA1980.DAT.*
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21: /SID88/gcgcdata/geneseq/geneseqn/NA2000.DAT.*
22: /SID88/gcgcdata/geneseq/geneseqn/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2967	100.0	2967	21	Human potassium ion
2	2967	100.0	3083	21	Human eag related
3	2795	94.2	2886	21	Human potassium ion
4	2795	94.2	3002	21	Human eag related
5	1294.4	43.6	2967	22	DNA encoding alpha
6	1294.4	43.6	3289	22	Human ether a gogo
7	432.2	14.6	1434	21	Human secreted pro
8	339.2	11.4	3479	22	Human HERC1 DNA
9	339.2	11.4	3480	21	Long QT syndrome a
10	339.2	11.4	3950	21	Long QT syndrome a
11	339.2	11.4	4070	22	Human eag-related

12	285.6	9.6	3355	21	AAZ50452	Human potassium c
13	281.8	9.5	3857	20	AAZ11906	Human potassium ch
14	281.4	9.5	3742	21	AAZ293334	Rat elk1 potassium
15	281.2	9.5	3249	21	AAZ50119	Human ELK voltage
16	281.2	9.5	3323	20	AAZ84910	Human brain specif
17	279.6	9.4	3829	21	AAZ87712	Human ESK1 (hesk1)
18	278	9.4	3252	21	AAZ14893	DNA encoding a her
19	272.8	9.2	3142	20	AAZ56416	Human erg subfam1
20	269.6	9.1	3715	20	AAZ84919	Rat brain specific
21	244.6	8.2	5107	21	AAZ50455	Human potassium ch
22	223.6	7.5	3064	20	AAZ84911	Human brain specif
23	218	7.3	3736	20	AAZ84918	Rat brain specif
24	205.8	6.9	3141	20	AAZ56415	Human erg subfam1
25	189	6.4	423	21	AAZ93336	Rat eag2 potassium
26	149.8	5.0	2694	21	AAZ50453	Human potassium ch
27	83	2.8	426	21	AAZ16301	Human kidney relat
28	80.8	2.7	1132	21	AAZ50454	Human potassium ch
29	76.8	2.6	487	22	AAZ13390	Probe #3323 for ge
30	76.8	2.6	487	22	AAZ13474	Probe #3430 used t
31	68.8	2.3	229	22	AAZ12619	Probe #12552 for g
32	68.8	2.3	229	22	AAZ17912	Probe #16598 used
33	66.8	2.3	1995	22	AAZ09558	Human transporter
34	66.6	2.2	470	22	AAZ14351	Probe #4284 for ge
35	66.6	2.2	470	22	AAZ15725	Human transferrin
36	66.6	2.2	470	22	AAZ10481	Probe #4172 used t
37	61.6	2.1	936	22	AAZ58252	Oligonucleotide D1
38	61.6	2.1	936	22	AAZ58254	Oligonucleotide D1
39	61.6	2.1	936	22	AAZ58257	Oligonucleotide D1
40	61.6	2.1	936	22	AAZ58259	Oligonucleotide D2
41	61.6	2.1	936	22	AAZ58262	Oligonucleotide D2
42	61.6	2.1	936	22	AAZ58255	Oligonucleotide D1
43	59.4	2.0	2888	20	AAZ09491	Human 1h ion chann
44	57.8	1.9	1820	20	AAZ09488	Bovine retina 1h 1
45	57.8	1.9	3431	22	AAZ98302	Human EST-derived

ALIGNMENTS

RESULT 1	
AAZ35717	
ID	AAZ35717 standard; cDNA; 2967 BP.
XX	
AC	AAZ35717;
XX	
DT	31-JAN-2000 (first entry)
XX	
DE	Human potassium ion eag channel protein encoding cDNA #2.
XX	
KW	Human; potassium ion eag channel; K+ ion channel; cancer; gene therapy;
KW	neurodegenerative disease; cell proliferation; diagnosis; tumour;
KW	psoriasis; neuroblastoma; cervix carcinoma; carcinoma;
KW	breast adenocarcinoma; breast carcinoma ductal type;
KW	Alzheimer's disease; Parkinson's disease; multiple sclerosis;
KW	lateral amyotrophic sclerosis; ds.
XX	
OS	Homo sapiens.
XX	
PN	W09954463-A2.
XX	
PD	28-OCT-1999.
XX	
PF	21-APR-1999; 99WO-EP02695.
XX	
PR	21-APR-1998; 98EP-0107268.
XX	
PA	(PLAC) MAX PLANCK GES FORDERUNG WISSENSCHAFTEN.
XX	
PI	Pardo-Fernandez IA, Stuehmer W, Beckh S, Brueggemann A;
XX	Del Camino Fernandez-Miranda D, Sanchez Perez A, Weseloh R;
DR	WPI; 2000-013250/01.
DR	P-PSDB; AAZ9945.

XX New gene encoding human ion channel useful for diagnosis of, e.g.
 PT cancer and neurodegenerative diseases -
 XX
 PS Claim 1; Page 88-89; 89pp; English.

CC The present sequence encodes a protein (I) having a function of the human
 CC K⁺ (potassium) ion eaq channel. Analysis of the expression of the
 CC polynucleotide encoding the protein (I) having a function of the human
 CC K⁺ (potassium) ion eaq channel (II) or quantitative presence of
 CC (I) in cells of mammals such as human, rat or mouse is useful for
 CC prognosing cancer, neurodegenerative disease and psoriasis. Cancer
 CC includes neuroblastoma, cervix carcinoma or mamma carcinoma such as
 CC breast adenocarcinoma or breast carcinoma ductal type. Neurodegenerative
 CC disease includes Alzheimer's disease, Parkinson's disease, lateral
 CC amyotrophic sclerosis or multiple sclerosis. By introducing an inhibitor
 CC of the expression of (II) or an inhibitor or modifying agent of the
 CC malfunction of (I) or (II) into a mammal disease caused by undesired
 CC expression or overexpression of (II) or malfunction of (I) can be
 CC prevented or treated. Inhibitor of the expression of (II) or (I) is also
 CC useful for inhibiting cell proliferation. (II) can be used in gene
 CC therapy for inhibiting cell proliferation or disease such as cancer or
 CC psoriasis and is also useful for specifically detecting human eaq mRNA
 CC in tissues, by employing the Northern Blot technology. Diagnostic
 CC compositions are useful in detecting the onset or progress of diseases
 CC e.g. cancer related to the undesired expression or overexpression of (II)
 CC and also for detecting malfunction of (I). They are further useful for
 CC classification of tumours or the developmental status of tumour.

Sequence 2967 BP; 735 A; 725 C; 826 G; 681 T; 0 other;

Query Match 100.0%; Score 2967; DB 21; Length 2967;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 atgacacatgctggggcagagagggagctagtcgcccctcaacaacagcttctgagagt 60
 Qy 61 atgttctggcggtccatgataactaatttctgttggggaatgctcagatgtgacg 120
 Db 61 atgttctggcggtccatgataactaatttctgttggggaatgctcagatgtgacg 120
 Qy 121 cctattgtacagcaatgagatttctgcaagctgctgctacacagggcaaaagt 180
 Db 121 cctattgtacagcaatgagatttctgcaagctgctgctacacagggcaaaagt 180
 Qy 181 atgcaaaaaaacagcactgagtttatagtatgaggagagctgactgataaagacagatt 240
 Db 181 atgcaaaaaaacagcactgagtttatagtatgaggagagctgactgataaagacagatt 240
 Qy 241 gaaaagtgtggcaaacatttgagaactatgagatgaaattccttgaattctgtatc 300
 Db 241 gaaaagtgtggcaaacatttgagaactatgagatgaaattccttgaattctgtatc 300
 Qy 301 aagaagaacagagacacactgtgtgttcttcttgaaaattgttccaattcgaaacgaag 360
 Db 301 aagaagaacagagacacactgtgtgttcttcttgaaaattgttccaattcgaaacgaag 360
 Qy 361 gataaagtgtttatttcttctgcaacttgcagtaacaagcttcaaacagcaatt 420
 Db 361 gataaagtgtttatttcttctgcaacttgcagtaacaagcttcaaacagcaatt 420
 Qy 421 gaggaatgatactgtaaaagcttggggaagtctgctggctgacaagagcactgacaagc 480
 Db 421 gaggaatgatactgtaaaagcttggggaagtctgctggctgacaagagcactgacaagc 480
 Qy 481 agcaggggtgtcctgcagcagctgctcacaagctgcaaaaaagcgagaaatgttccacaag 540
 Db 481 agcaggggtgtcctgcagcagctgctcacaagctgcaaaaaagcgagaaatgttccacaag 540
 Qy 541 caatccgcctgagagagttcctacagctgggtcagacatccttccacagtaacaagaa 600

Db 541 caatccgcctgagagagttcctacagctgggtcagacatccttccacagtaacaagaa 600
 Qy 601 gaggcacaaagacccccctcacatcatatattgtgttttaagccaaagt 660
 Db 601 gaggcacaaagacccccctcacatcatatattgtgttttaagccaaagt 660
 Qy 661 gatgatacatcttattcttgaacctctatagacacattgtgcttataatgtctcc 720
 Db 661 gatgatacatcttattcttgaacctctatagacacattgtgcttataatgtctcc 720
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 Db 721 ttcaaaacagcagaataatgttggccttgcgtgtgttgaagacatcgttgatgtatc 780
 Qy 781 ttttgggtgagatgtgtctcaatttctataccacttgttggagacaaagggagtg 840
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 Db 841 attctgaccccaacttaccgcatgaactaccctgaagcgtgtgttgatgtacct 900
 Qy 901 ctgtcctgtttgcatalatgtatcacaagccttctgagaacgtgagatgagttatgccc 960
 Db 901 ctgtcctgtttgcatalatgtatcacaagccttctgagaacgtgagatgagttatgccc 960
 Qy 961 ttataggtatccagaggagagattgttctgtatcacaattccaccaccactggagg 1020
 Db 961 ttataggtatccagaggagagattgttctgtatcacaattccaccaccactggagg 1020
 Qy 1021 aagaagagtcagagcatcagcagcagcctgttcagctcctctctctctctctctct 1080
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 Db 1081 ctgtggcagatgtgcccgttaagcttggacacatcatgaaatgagctgtgtctgtc 1140
 Qy 1141 ctgtcgtgtgtgtgttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1200
 Db 1141 ctgtcgtgtgtgtgttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1200
 Qy 1201 ggggactatgagatcttctacagagacacacacacacacacacacacacacacac 1260
 Db 1201 ggggactatgagatcttctacagagacacacacacacacacacacacacacacac 1260
 Qy 1261 caactagcagatgagatcttctacacacacacacacacacacacacacacacac 1320
 Db 1261 caactagcagatgagatcttctacacacacacacacacacacacacacacacac 1320
 Qy 1321 gaagtgtgtcccaagaagaattctgtctatcactctctgtgtgtgtgtgtgtgtgt 1380
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 Db 1681 aagagacatgagcgacgcacatctgctgacactgaaacgcgcaagtgcttcaagagacccg 1740
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 Db 1741 ggcctccggtgagcgaatgtagtgcctccggcgcacgtgaggtttcaagaagtg 1800
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 Db 2221 ttccagagatctccagacagaaagagcgagctgtagcagtgagagaggggagcgagac 2280
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 Db 2341 agcctctggaagcgacggtgacccgtgtgagagctcctgacagcccgatctcttc 2400
 Qy 2401 caggcagccctccacctccggggtgcccagacagcaagctacagggcgccaggtccgag 2460
 Db 2401 caggcagccctccacctccggggtgcccagacagcaagctacagggcgccaggtccgag 2460
 Qy 2461 tgcctgggcccccaagggggcgggcgatgtgccaagcgcaaaagctgggccccgctc 2520
 Db 2461 tgcctgggcccccaagggggcgggcgatgtgccaagcgcaaaagctgggccccgctc 2520
 Qy 2521 aaagatgcttgcggggaagatgtagactgtgaaagaagtgtccaagctgtagtgaagag 2580
 Db 2521 aaagatgcttgcggggaagatgtagactgtgaaagaagtgtccaagctgtagtgaagag 2580
 Qy 2581 aacactccagagagaaagaagcgtcagggcgagggccacacgtgaagaagacagactcgtgt 2640
 Db 2581 aacactccagagagaaagaagcgtcagggcgagggccacacgtgaagaagacagactcgtgt 2640
 Qy 2641 gaaagtgatcaacaaagacgactgtgctctgacaacagtgggtgagcagagatccc 2700
 Db 2641 gaaagtgatcaacaaagacgactgtgctctgacaacagtgggtgagcagagatccc 2700
 Qy 2701 cagagatcgagctccatctctgacagagtgcaagcatcgttctaccccatctctgagag 2760
 Db 2701 cagagatcgagctccatctctgacagagtgcaagcatcgttctaccccatctctgagag 2760

Qy 2761 acgtcgcagggccacagctctctgtaggtgagcagcgactgaagaagagacatcaagcctta 2820
 Db 2761 acgtcgcagggccacagctctctgtaggtgagcagcgactgaagaagagacatcaagcctta 2820
 Qy 2821 aacgccaatgaccatattgagaagaagcgtctcgtgaatactcagatataacttcc 2880
 Db 2821 aacgccaatgaccatattgagaagaagcgtctcgtgaatactcagatataacttcc 2880
 Qy 2881 agaagatcctcagctctcctcagagatgtgttgaataatcgaagccacagctcccaaga 2940
 Db 2881 agaagatcctcagctctcctcagagatgtgttgaataatcgaagccacagctcccaaga 2940
 Qy 2941 tcagagagagacatttttgagagcagc 2967
 Db 2941 tcagagagagacatttttgagagcagc 2967

RESULT 2
 AA235722
 ID AA235722 standard; cDNA: 3083 BP.
 XX
 AC AA235722;
 XX
 DT 31-JAN-2000 (first entry)
 XX
 DE Human eag related gene nucleotide sequence #2.
 XX
 KW Human: potassium ion eag channel; K+ ion channel; cancer; gene therapy;
 KW neurodegenerative disease; cell proliferation; diagnosis; tumour;
 KW psoriasis; neuroblastoma; cervix carcinoma; carcinoma;
 KW breast adenocarcinoma; breast carcinoma ductal type;
 KW Alzheimer's disease; Parkinson's disease; multiple sclerosis;
 KW lateral amyotrophic sclerosis; ds.
 KW
 XX Homo sapiens.
 XX
 OS WO954463-A2.
 XX
 PN 28-OCT-1999.
 XX
 PD 21-APR-1999; 99WO-EP02695.
 XX
 PF 21-APR-1998; 98EP-0107268.
 XX
 PR (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 PA Pardo-Fernandez LA, Stuehmer W, Beckh S, Brueggemann A;
 PI Del Camino Fernandez-Miranda D, Sanchez Perez A, Weseloh R;
 DR MPI: 2000-013250/01.
 XX
 XX
 PT New gene encoding human ion channel useful for diagnosis of, e.g.
 PT cancer and neurodegenerative diseases -
 PT
 PS Example 1; Page 73-75; 89pp; English.
 XX
 CC The present invention describes proteins (I) having a function of the
 CC human K+ (potassium) ion eag channel. Analysis of the expression of the
 CC polynucleotide encoding the protein (I) having a function of the human
 CC K+ (potassium) ion eag channel (II) or quantitative presence of
 CC (I) in cells of mammals such as human, rat or mouse is useful for
 CC prognosing cancer, neurodegenerative disease and psoriasis. Cancer
 CC includes neuroblastoma, cervix carcinoma or mamma carcinoma such as
 CC breast adenocarcinoma or breast carcinoma ductal type. Neurodegenerative
 CC disease includes Alzheimer's disease, Parkinson's disease, lateral
 CC amyotrophic sclerosis or multiple sclerosis. By introducing an inhibitor
 CC of the expression of (II) or an inhibitor or modifying agent of the
 CC malfunction of (I) or (II) into a mammal disease caused by undesired
 CC expression or overexpression of (II) or malfunction of (I) can be
 CC prevented or treated. Inhibitor of the expression of (II) or (I) is also
 CC useful for inhibiting cell proliferation. (II) can be used in gene
 CC therapy for inhibiting cell proliferation or disease such as cancer or

CC psoriasis and is also useful for specifically detecting human ead mRNA
CC in tissues, by employing the Northern Blot technology. Diagnostic
CC compositions are useful in detecting the onset or progress of diseases
CC e.g. cancer related to the undesired expression or overexpression of (11)
CC and also for detecting malfunction of (1). They are further useful for
CC classification of tumours or the developmental status of tumour. The
CC present sequence represents a human ead related gene (HENG) nucleotide
CC Sequence from the present invention.

XX Sequence 3083 BP; 767 A; 765 C; 852 G; 699 T; 0 other;

Query Match 100.0%; Score 2967; DB 21; Length 3083;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2967; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atgaccatgctgggggagggagggagtagtggccctcaaaacagttcttgagat 60
DB 37 atgaccatgctgggggagggagggagtagtggccctcaaaacagttcttgagat 96
OY 61 atgttcgcgctccaatgatactaatttgttggggaatgctcagatagtgactg 120
DB 97 attgttcgcgctccaatgatactaatttgttggggaatgctcagatagtgactg 156
OY 121 cctattgttacaagaatgatggaatttgcgaagctgtctgctacacagggcagaagt 180
DB 157 cctattgttacaagaatgatggaatttgcgaagctgtctgctacacagggcagaagt 216
OY 181 atgcaaaaagcagacactgacatttattgtatggggagctgactgataaagacgatt 240
DB 217 atgcaaaaagcagacactgacatttattgtatggggagctgactgataaagacgatt 276
OY 241 gaaaagtgccgcaacatttgagaaactatgagatgaaattccttgaaatttgatgac 300
DB 277 gaaaagtgccgcaacatttgagaaactatgagatgaaattccttgaaatttgatgac 336
OY 301 aagaagaacagagacactgtgtgtgttcttcttgtaaaattgtctcaattcgaacagacag 360
DB 337 aagaagaacagagacactgtgtgtgttcttcttgtaaaattgtctcaattcgaacagacag 396
OY 361 gataaagtggtttatttcttcttgacatttcagtgacataacagcttccaagaacgaatt 420
DB 397 gataaagtggtttatttcttcttgacatttcagtgacataacagcttccaagaacgaatt 456
OY 421 gagatgatactatgaagaagctggggagagttgtctcgctcagacaagaagcactgtgacaag 480
DB 457 gagatgatactatgaagaagctggggagagttgtctcgctcagacaagaagcactgtgacaag 516
OY 481 agcaggggtgtctctcagcagcgtgtctccaagcgtgcacaanaagcgagatgtccacaag 540
DB 517 agcaggggtgtctctcagcagcgtgtctccaagcgtgtgcacaanaagcgagatgtccacaag 576
OY 541 cacttcgcgcctggcagaggtctctaagctgggtcagacatcctcccaagtacaagcaa 600
DB 577 cacttcgcgcctggcagaggtctctaagctgggtcagacatcctcccaagtacaagcaa 636
OY 601 gaggcaccaagaagactccctccacatcatcttacaatttggttttaaagccagctgag 660
DB 637 gaggcaccaagaagactccctccacatcatcttacaatttggttttaaagccagctgag 696
OY 661 gatlgatcatcttgatcttgacactctatacagcactcttgctccctataatgtctcc 720
DB 697 gatlgatcatcttgatcttgacactctatacagcactcttgctccctataatgtctcc 756
OY 721 ttcaaaacagcagagaataatgtgctgtgctgtgtgtatgatacgttgatgtctatc 780
DB 757 ttcaaaacagcagagaataatgtgctgtgctgtgtgtatgatacgttgatgtctatc 816
OY 781 ttttggggagcatgtgtctcaatttataccacatttgggaccgcaaggagggtg 840
DB 817 ttttggggagcatgtgtctcaatttataccacatttgggaccgcaaggagggtg 876
OY 841 attctgcaccaaatataccgcatgaaactcgaagaagctggtttgtgtgacatt 900

DB 877 attctgcaccaaatataccgcatgaaactcgaagaagctggtttgtgtgacatt 936
OY 901 ctgtcctgtttgcataatgatgtcatcaacgcttttgaaacgttgatgattgctgc 960
DB 937 ctgtcctgtttgcataatgatgtcatcaacgcttttgaaacgttgatgattgctgc 996
OY 961 ttatagtgtatccaggagaaattgtttgtgtatcaaatccaccactggagagg 1020
DB 997 ttatagtgtatccaggagaaattgtttgtgtatcaaatccaccactggagagg 1056
OY 1021 agagagatcagaagcagacacagcagctgttcaacgtctcttaaaagtgtccgctgcct 1080
DB 1057 agagagatcagaagcagacacagcagctgttcaacgtctcttaaaagtgtccgctgcct 1116
OY 1081 ctgtgcagatggcccgtaagctgtgacacactacatgtaataatgagctgtgtgcctgc 1140
DB 1117 ctgtgcagatggcccgtaagctgtgacacactacatgtaataatgagctgtgtgcctgc 1176
OY 1141 ctgtgcagatggctgtttgt 1200
DB 1177 ctgtgcagatggctgtttgt 1236
OY 1201 ggggactatgagatcttgaacagagacacacagaaatccgcacaacagctgtgtac 1260
DB 1237 ggggactatgagatcttgaacagagacacacagaaatccgcacaacagctgtgtac 1296
OY 1261 caactagcagatgagatcttgaacagagacacacagaaatccgcacaacagctgtgtac 1320
DB 1297 caactagcagatgagatcttgaacagagacacacagaaatccgcacaacagctgtgtac 1356
OY 1321 gaagtggtgcccaagaagatctgtctacatctctgtgtgtgtgtgtgtgtgtgtgtgt 1380
DB 1357 gaagtggtgcccaagaagatctgtctacatctctgtgtgtgtgtgtgtgtgtgtgtgt 1416
OY 1381 ctcaaccagtgtggtcttgggaacatcgcccatccacagacattgagaagatcttgca 1440
DB 1417 ctcaaccagtgtggtcttgggaacatcgcccatccacagacattgagaagatcttgca 1476
OY 1441 gttggcattatgattgt 1500
DB 1477 gttggcattatgattgt 1536
OY 1501 atttccacaagatgatactgac 1560
DB 1537 atttccacaagatgatactgac 1596
OY 1561 gacttcctgaagctctacacaggtgtccaaaagagattgagtgagcagtaattatatt 1620
DB 1597 gacttcctgaagctctacacaggtgtccaaaagagattgagtgagcagtaattatatt 1656
OY 1621 gtttcactgtgtccatgtgtccagagcatttgacacagaaagcttcttgagattctccc 1680
DB 1657 gtttcactgtgtccatgtgtgtccagagcatttgacacagaaagcttcttgagattctccc 1716
OY 1681 aaggacatgagccagacactgt 1740
DB 1717 aaggacatgagccagacactgt 1776
OY 1741 gcttccgctgtgcaagtgatgt 1800
DB 1777 gcttccgctgtgcaagtgatgt 1836
OY 1801 cactgt 1860
DB 1837 cactgt 1896
OY 1861 gttgttctgt 1920
DB 1897 gttgttctgt 1956
OY 1921 gttgttctgt 1980

```
Db 1957 ggaagcgttttgagatgtgttctggaaggaagcacccttgcacgttcctgtccaat 2016
Qy 1981 gttgagccttgacctactgtgatctgcatgtgatcaagcgggagatgcctgcagaagt 2040
Db 2017 gttgagccttgacctactgtgatctgcatgtgatcaagcgggagatgcctgcagaagt 2076
Qy 2041 ctggaattctcaagcgccttccatctcttccctgcgaacctgtatcttgacataaac 2100
Db 2077 ctggaattctcaagcgccttccatctcttccctgcgaacctgtatcttgacataaac 2136
Qy 2101 ttgaggaagagatgtgttctcgaagaatcagcgaatgtgaaacgagaaagaaacac 2160
Db 2137 ttgaggaagagatgtgttctcgaagaatcagcgaatgtgaaacgagaaagaaacac 2196
Qy 2161 atgaacgaagaatgagccccctgatacttgcgcccgagcaacctgttcggcgctc 2220
Db 2197 atgaacgaagaatgagccccctgatacttgcgcccgagcaacctgttcggcgctc 2256
Qy 2221 ttccaagatctccgacagcaaaagagagccagctgcagctgaaagagggcgccggagc 2280
Db 2257 ttccaagatctccgacagcaaaagagagccagctgcagctgaaagagggcgccggagc 2316
Qy 2281 ctggaataccatggtgtgagaagaagcaatgtccttacagagcatgcctccgcaaacac 2340
Db 2317 ctggaataccatggtgtgagaagaagcaatgtccttacagagcatgcctccgcaaacac 2376
Qy 2341 agctctgtgaagcgaagctgtgtacacgtgtcgtgagagctccctgcacgcccctatcctc 2400
Db 2377 agctctgtgaagcgaagctgtgtacacgtgtcgtgagagctccctgcacgcccctatcctc 2436
Qy 2401 caggcaagcctccacccctccgggtgtccagacaacgaagctacagggcgccaggttccag 2460
Db 2437 caggcaagcctccacccctccgggtgtccagacaacgaagctacagggcgccaggttccag 2496
Qy 2461 tgcctggggcccaagggggggggggcgatgtgtgccaagcgaaagcgtggccggcttc 2520
Db 2497 tgcctggggcccaagggggggggggcgatgtgtgccaagcgaaagcgtggccggcttc 2556
Qy 2521 aaagatccttcgsgaaagagtgagagctgtaaacaggtgtccaaagctgtgagctgtgag 2580
Db 2557 aaagatccttcgsgaaagagtgagagctgtaaacaggtgtccaaagctgtgagctgtgag 2616
Qy 2581 acacttcccgagagacaacaaacgttcagggcgagggccacactgaaagaacagactcgtgt 2640
Db 2617 acacttcccgagagacaacaaacgttcagggcgagggccacactgaaagaacagactcgtgt 2676
Qy 2641 gacagtggcatcaccaagagagcttgcctgtgacaacgtgtggtgagggccagggctcc 2700
Db 2677 gacagtggcatcaccaagagagcttgcctgtgacaacgtgtggtgagggccagggctcc 2736
Qy 2701 cagatcggaatcccatctcctgcagaggttcaagactcgttctaccccatccctgagcag 2760
Db 2737 cagatcggaatcccatctcctgcagaggttcaagactcgttctaccccatccctgagcag 2796
Qy 2761 acgtctcagggccacagctctgaggtgaggtgagcagagctgtaaggaagagacatcaaggccta 2820
Db 2797 acgtctcagggccacagctctgaggtgaggtgagcagagctgtaaggaagagacatcaaggccta 2856
Qy 2821 aacgcacaaatgacacaataatgtgagaacagctctctgagatacttaagatatattcc 2880
Db 2857 aacgcacaaatgacacaataatgtgagaacagctctctgagatacttaagatatattcc 2916
Qy 2881 agaagatcctctcagcttccctcagagagtgttgaatatcagggccacagctccacaga 2940
Db 2917 agaagatcctctcagcttccctcagagagtgttgaatatcagggccacagctccacaga 2976
Qy 2941 tcagagagagacatttttgagcagc 2967
Db 2977 tcagagagagacatttttgagcagc 3003
```

RESULT 3
AAZ35716

```
ID AAZ35716 standard; cDNA; 2886 BP.
XX
AC AAZ35716;
XX
DT 31-JAN-2000 (first entry)
XX
DE Human potassium ion eag channel protein encoding cDNA #1.
XX
KW Human; potassium ion eag channel; K+ ion channel; cancer; gene therapy;
KW neurodegenerative disease; cell proliferation; diagnosis; tumour;
KW psoriasis; neuroblastoma; cervix carcinoma; carcinoma;
KW breast adenocarcinoma; breast carcinoma ductal type;
KW Alzheimer's disease; Parkinson's disease; multiple sclerosis;
KW lateral amyotrophic sclerosis; ds.
XX
OS Homo sapiens.
XX
PN MO954463-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99MO-EP02695.
XX
PR 21-APR-1998; 98BP-0107268.
XX
PA (PLAC ) MAX PLANCK GBS FOERDERUNG WISSENSCHAFTEN.
PI Pardo-Fernandez LA, Stuehmer W, Beckh S, Brueggemann A;
PI Del Camino Fernandez-Miranda D, Sanchez Perez A, Weseloh R;
XX
DR WPI: 2000-013250/01.
DR P-PSDB: AAY49944.
XX
PT New gene encoding human ion channel useful for diagnosis of, e.g.
XX cancer and neurodegenerative diseases -
XX
PS Claim 1: Page 85-87; 89pp; English.
XX
CC The present sequence encodes a protein (I) having a function of the human
CC K+ (potassium) ion eag channel. Analysis of the expression of the
CC polynucleotide encoding the protein (I) having a function of the human
CC K+ (potassium) ion eag channel (II) or quantitative presence of
CC (I) in cells of mammals such as human, rat or mouse is useful for
CC prognosing cancer, neurodegenerative disease and psoriasis. Cancer
CC includes neuroblastoma, cervix carcinoma or mamma carcinoma such as
CC breast adenocarcinoma or breast carcinoma ductal type. Neurodegenerative
CC disease includes Alzheimer's disease, Parkinson's disease, lateral
CC amyotrophic sclerosis or multiple sclerosis. By introducing an inhibitor
CC of the expression of (II) or an inhibitor or modifying agent of the
CC malfunction of (I) or (II) into a mammal disease caused by undesired
CC expression or overexpression of (II) or malfunction of (I) can be
CC prevented or treated. Inhibitor of the expression of (II) or (I) is also
CC useful for inhibiting cell proliferation. (II) can be used in gene
CC therapy for inhibiting cell proliferation or disease such as cancer or
CC psoriasis and is also useful for specifically detecting human eag mRNA
CC in tissues, by employing the Northern Blot technology. Diagnostic
CC compositions are useful in detecting the onset or progress of diseases
CC e.g. cancer related to the undesired expression or overexpression of (II)
CC and also for detecting malfunction of (I). They are further useful for
CC classification of tumours or the developmental status of tumour.
XX
SQ Sequence 2886 BP; 716 A; 711 C; 799 G; 660 T; 0 other;

Query Match          94.2%; Score 2795; DB 21; Length 2886;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 2886; Conservative 0; Mismatches 0; Indels 81; Gaps 1;
```

Qy 1 atgacatggttggtggggagggaggtgtgtcccttaaaacagtttttggaagt 60
Db 1 atgacatggttggtggggagggaggtgtgtcccttaaaacagtttttggaagt 60
Qy 61 atgttcggtggccaatgatactattgtgtgtgggaatgtcagatagtgtgactgg 120

Db	61	attgttcg	cggtcc	aaatga	taccta	attctt	gcttg	gggaat	gctcaga	tacga	tacg	gagct	g	120		
Oy	121	cc	atctgtg	tacaga	caatgat	tgatatt	tgtc	caagctgtc	gcgc	atca	caag	gcaga	agt	180		
Db	121	cc	atctgtg	tacaga	caatgat	tgatatt	tgtc	caagctgtc	gcgc	atca	caag	gcaga	agt	180		
Oy	181	at	gc	aaaaaa	agcag	caac	ctgc	agatt	tatgat	atg	ggga	gcgtgc	atgata	agacagat	240	
Db	181	at	gc	aaaaaa	agcag	caac	ctgc	agatt	tatgat	atg	ggga	gcgtgc	atgata	agacagat	240	
Oy	241	g	aaaaag	tgcgc	caacatt	ttaga	actatg	agata	atcc	ttc	ttga	atcc	tgcgat	g	300	
Db	241	g	aaaaag	tgcgc	caacatt	ttaga	actatg	agata	atcc	ttc	ttga	atcc	tgcgat	g	300	
Oy	301	a	agaaga	acag	agacac	ctctgt	gtgtct	cttgc	tbaa	aatgt	ctcca	atctga	aaacg	acag	360	
Db	301	a	agaaga	acag	agacac	ctctgt	gtgtct	cttgc	tbaa	aatgt	ctcca	atctga	aaacg	acag	360	
Oy	361	g	ataa	agtg	ttt	atctt	ctctgc	actt	ccag	tgcata	aaacag	cttca	aaacg	ccaat	420	
Db	361	g	ataa	agtg	ttt	atctt	ctctgc	actt	ccag	tgcata	aaacag	cttca	aaacg	ccaat	420	
Oy	421	g	gg	ggtat	ctac	tgt	taaa	ggctgc	gggga	agttt	gctc	gcgtgc	ta	caagagac	480	
Db	421	g	gg	ggtat	ctac	tgt	taaa	ggctgc	gggga	agttt	gctc	gcgtgc	ta	caagagac	480	
Oy	481	a	gc	ag	ggg	gtctc	ctgc	agac	gcgtgc	gtcc	aaag	gcg	gaatgt	ccacaag	540	
Db	481	a	gc	ag	ggg	gtctc	ctgc	agac	gcgtgc	gtcc	aaag	gcg	gaatgt	ccacaag	540	
Oy	541	c	actcc	ccgc	ctgc	g	aga	ggtgc	tc	taca	gcgtgc	gtgc	tc	agacalc	600	
Db	541	c	actcc	ccgc	ctgc	g	aga	ggtgc	tc	taca	gcgtgc	gtgc	tc	agacalc	600	
Oy	601	g	gg	gc	ca	ccca	aa	gaac	ctcc	ctca	catc	at	tgtgt	ttta	agacag	660
Db	601	g	gg	gc	ca	ccca	aa	gaac	ctcc	ctca	catc	at	tgtgt	ttta	agacag	660
Oy	661	g	at	tgc	at	catc	tgt	at	ctgc	actc	tca	ag	ccac	ctctgt	gc	720
Db	661	g	at	tgc	at	catc	tgt	at	ctgc	actc	tca	ag	ccac	ctctgt	gc	720
Oy	721	t	tca	aa	ac	ca	g	ga	ta	atgt	gc	gc	tgc	gtgt	gt	780
Db	721	t	tca	aa	ac	ca	g	ga	ta	atgt	gc	gc	tgc	gtgt	gt	780
Oy	781	t	t	t	t	t	t	t	t	t	t	t	t	t	t	840
Db	781	t	t	t	t	t	t	t	t	t	t	t	t	t	t	840
Oy	841	a	t	t	t	t	t	t	t	t	t	t	t	t	t	900
Db	841	a	t	t	t	t	t	t	t	t	t	t	t	t	t	900
Oy	901	c	t	t	t	c	c	t	t	c	a	t	g	a	t	960
Db	901	c	t	t	c	c	t	t	c	a	t	g	a	t	g	960
Oy	961	t	t	t	a	t	g	t	g	t	c	a	g	a	g	1020
Db	961	t	t	t	a	t	g	t	c	a	g	a	g	a	g	1020
Oy	1021	a	g	a	g	a	g	a	g	a	g	a	g	a	g	1080
Db	950	-----	a	g	g	a	g	a	g	a	g	a	g	a	g	999
Oy	1081	c	t	t	t	g	c	c	g	a	t	g	a	g	c	1140
Db	1000	c	t	t	t	g	c	c	g	a	t	g	a	g	c	1059
Oy	1141	c	t	t	t	g	c	c	g	a	t	g	a	g	c	1200

[illegible]

OY	2261	ctgtaactagatgattggaagaaggcaattgtctcttacagagcatgtcctccgccaacac	2340
Db	2200	cttgatctgacctagatgtgtgaaagaggcaattgtctcttacagagcatgtcctccgccaacac	2259
-OY	2341	agccctcgtaagaagccaagcgtgtgtcaacggtgctgtgaagatctctgcacgcccgtatcttc	2400
Db	2260	agccctcgtaagaagccaagcgtgtgtcaacggtgctgtgaagatctctgcacgcccgtatcttc	2319
OY	2401	caagcagccctccacactcccggtgtgcacagaccacacgtccaaagctaaagcgcgcgaagttccag	2460
Db	2320	caagcagcactccacactcccggtgtgcacagaccacagctaaagcgcgcgaagttccag	2379
OY	2461	tgcctgtgcccccaaggggtggtgcggtgcgattgtgtccaaagcgaagaagctgtgcccgttc	2520
Db	2380	tgcctgtgcccccaaggggtggtggtgcgattgtgtgtccaaagcgaagaagctgtgcccgttc	2439
OY	2521	aaagatgtctgtggtgaagaaggtgaagacttgaaacaaggtgtccaaagctgaatcgtatggaag	2580
Db	2440	aaagatgtctgtggtgaagaaggtgaagacttgaaacaaggtgtccaaagctgtatcgtatggaag	2499
●	2581	acaactcccgaaagagacaacaagaagcttcaggtcgaggtccacactgtgaagaagaacagatcgtgt	2640
Db	2500	acaactcccgaaagagacaacaagaagcttcaggtcgaggtccacactgtgaagaagaacagatcgtgt	2559
OY	2641	gacaaatgtgcataccaacaagagcgacttgccctgtgacaacgtgtgtgtgaagccaaagtctcc	2700
Db	2560	gacaaatgtgcataccaacaagagcgacttgccctgtgacaacgtgtgtgtgaagccaaagtctcc	2619
OY	2701	caaggtctgagatcccatctctgtgcagaaggtccaagcattcgttccaccatccctgtgacag	2760
Db	2620	caaggtctgagatcccatctctgtgtcagaaggtccaagcattcgttccaccatccctgtgacag	2679
OY	2761	acgtctgcaggtccacagctctctgtgaagtgtgaagtcacagcagctgaagaagagacatcaagcgctta	2820
Db	2680	acgtctgcaggtccacagctctctgtgaagtgtgaagtcacagcagctgaagaagagacatcaagcgctta	2739
OY	2821	aacgtccaaatgaaccaaatatttgaagaacagctctctcgtagatatactcaagatatctaacttc	2880
Db	2740	aacgtccaaatgaaccaaatatttgaagaacagctctctcgtagatatactcaagatatctaacttc	2799
OY	2881	agaagaatcctcctcagctctcctcaagaggtgtgttgaatatcgagtcacagtcaccagaa	2940
Db	2800	agaagaatcctcctcagctctcctcaagaggtgtgttgaatatcgagtcacagtcaccagaa	2859
OY	2941	tcaagagagagacattttgtgagccagc	2967
Db	2860	tcaagagagagacattttgtgagccagc	2886
●	4		
AAZ35721			
ID	AAZ35721	standard; cDNA; 3002 BP.	
XX	AAZ35721;		
DE	31-JAN-2000	(first entry)	
XX			
DE	Human eag related gene nucleotide sequence #1.		
XX			
KW	Human; potassium ion eag channel; K+ ion channel; cancer; gene therapy		
KW	neurodegenerative disease; cell proliferation; diagnosis; tumour;		
KW	psoriasis; neuroblastoma; cervix carcinoma; carcinoma;		
KW	breast adenocarcinoma; breast carcinoma ductal type;		
KW	Alzheimer's disease; Parkinson's disease; multiple sclerosis;		
KW	lateral amyotrophic sclerosis; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	W09954463-A2.		
XX			
XX	28-OCT-1999.		
DD			

PE 21-APR-1999; 99WO-EP02695.
XX
PR 21-APR-1998; 98EP-0107268.
XX
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
XX Pardo-Fernandez LA, Stuehmer W, Beckh S, Brueggemann A;
PI Del Camino Fernandez-Miranda D, Sanchez Perez A, Weseloh R;
XX
XX WPI; 2000-013250/01.
DR
XX
XX New gene encoding human ion channel useful for diagnosis of, e.g.
PT cancer and neurodegenerative diseases -
XX
XX Example 1; Page 71-73; 89pp; English.
PS

The present invention describes proteins (I) having a function of the human K⁺ (potassium) ion eeg channel. Analysis of the expression of the polynucleotide encoding the protein (I) having a function of the human K⁺ (potassium) ion eeg channel (II) or quantitative presence of (I) in cells of mammals such as human, rat or mouse is useful for prognosing cancer, neurodegenerative disease and psoriasis. Cancer includes neuroblastoma, cervix carcinoma or mamma carcinoma such as breast adenocarcinoma or breast carcinoma ductal type. Neurodegenerative disease includes Alzheimer's disease, Parkinson's disease, lateral amyotrophic sclerosis or multiple sclerosis. By introducing an inhibitor of the expression of (II) or an inhibitor or modifying agent of the malfunction of (I) or (II) into a mammal disease caused by undesired expression or overexpression of (II) or malfunction of (I) can be prevented or treated. Inhibitor of the expression of (II) or (I) is also useful for inhibiting cell proliferation. (II) can be used in gene therapy for inhibiting cell proliferation or disease such as cancer or psoriasis and is also useful for specifically detecting human eeg mRNA in tissues, by employing the Northern Blot technology. Diagnostic compositions are useful in detecting the onset or progress of diseases e.g. cancer related to the undesired expression or overexpression of (II) and also for detecting malfunction of (I). They are further useful for classification of tumours or the developmental status of tumour. The present sequence represents a human eeg related gene (HERG) nucleotide sequence from the present invention.

Sequence 3002 BP; 748 A; 751 C; 825 G; 678 T; 0 other;

Query Match 94.28; Score 2795; DB 21; Length 3002;

```

Best Local Similarity  97.38;  Pieu. NO. 0;
Matches 2886;  Conservative  0;  Mismatches  0;  Indels  81;  Gaps  1;

```

Qy	1	atgaccatgctctgggagcaggaaggagctagctggccctcaaaacagtttcttggagaat	60
Db	37	atgaccatgctctgggagcaggaaggagctagctggccctcaaaacagtttcttggagaat	96
Oy	61	atgtctcgcgccccaatgatactaatcttctgttgggaaatgtctaatgtatgtgacttg	120
Db	97	atgtctcgcgccccaatgatactaatcttctgttgggaaatgtctaatgtatgtgacttg	156
Oy	121	cctattgtgtacgaagaatgatgattcttctgcaagctctgtctgtctatccacaggcagaatg	180
Db	157	cctattgtgtacgaagaatgatgattcttctgcaagctctgtctgtctatccacaggcagaatg	216
Oy	181	atgcataaaaagcagcacctctgcagtttatgtatgtatgggagctgtacgtataagaacagat	240
Db	217	atgcataaaaagcagcacctctgcagtttatgtatgtatgggagctgtacgtataagaacagat	276
Oy	241	gaaaaagctgcgcaaacatttgagaactatgatatgaattcccttgaattctgatatc	300
Db	277	gaaaaagctgcgcaaacatttgagaactatgatatgaattcccttgaattctgatatc	336
Oy	301	aagaagaacaggaacacctgtgttcttctgtgaaatgtgtccaatttgtaaaagcaacag	360
Db	337	aagaagaacaggaacacctgtgttcttctgtgaaatgtgtccaatttgtaaaagcaacag	396
Oy	361	gataaagctggtttatcttcttgcacttgcataaataaagaattccaacacacatt	420


```
QY 2581 acacttcgcagagagacaaaagctcagggagggccacactgtgaagaagacagactcgtgt 2640
    |||
Db 2536 acacttcgcagagagacaaaagctcagggagggccacactgtgaagaagacagactcgtgt 2595
- QY 2641 gaaagtgcatacacaagagagacttcgcctgtgacacaacgtgggtgaagcagagatccc 2700
    |||
Db 2596 gaaagtgcatacacaagagagacttcgcctgtgacacaacgtgggtgaagcagagatccc 2655
QY 2701 cagagatcggatccatccctcctgcagagaggtcgaagatcgttctacatcccatccctgagag 2760
    |||
Db 2656 cagagatcggatccatccctcctgcagagaggtcgaagatcgttctacatcccatccctgagag 2715
QY 2761 acgtcgcagggccacagctcctcggaggtgtagggcagagctgtaagsgagacatcaaggcctta 2820
    |||
Db 2716 acgtcgcagggccacagctcctcggaggtgtagggcagagctgtaagsgagacatcaaggcctta 2775
QY 2821 aagcgccaaatgtgccaatatttgagaacaagctcctgtagatactcagatatttaactcc 2880
    |||
Db 2776 aagcgccaaatgtgccaatatttgagaacaagctcctgtagatactcagatatttaactcc 2835
    2881 aagaatcctcctcagctcctcctcagaggtgtgttgaataatcagagccacagctcccaagaa 2940
    |||
Db 2836 aagaatcctcctcagctcctcctcagaggtgtgttgaataatcagagccacagctcccaagaa 2895
QY 2941 tcagagagagacatlttttgagagccagc 2967
    |||
Db 2896 tcagagagagacatlttttgagagccagc 2922

RESULT 5
AAF25271
ID AAF25271 standard; DNA; 2967 BP.
XX
AC AAF25271;
XX
DT 30-APR-2001 (first entry)
XX
DE DNA encoding alpha-subunit of voltage-gated potassium channel (Eag2).
XX
KW Alpha-subunit; voltage-gated potassium channel; Eag2; ion flux;
KW central nervous system disorder; migraine; hearing; vision; stroke;
KW Alzheimer's disease; memory disorder; seizure; psychotic disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2967
    /tag=a
    /product="Eag2"
PN MO200104133-A1.
XX
PD 18-JAN-2001.
XX
PE 12-JUL-2000; 2000MOW-US18898.
XX
PR 13-JUL-1999; 99US-0143467.
XX
PA (ICAG-) ICAGEN INC.
XX
PI Jiegla TJ, Liu Y;
XX
DR MPI: 2001-138308/14.
XX
P-PSDB; AAB31714.
XX
PT Novel alpha subunit of potassium channel for identifying modulators of
    the channel for use in treating disorders involving abnormal ion flux,
    e.g. central nervous system disorders -
XX
PS Claim 6; Page 60; 75pp; English.
XX
CC The present sequence encodes an alpha-subunit of a voltage-gated
```

```
CC potassium channel. The polypeptide is designated Eag2. The polypeptide
CC is useful for screening activators or inhibitors of voltage-gated
CC potassium channels that contain an Eag2 subunit. Modulators of
CC voltage-gated channel activity are useful for treating disorders
CC involving abnormal ion flux, e.g. central nervous system (CNS)
CC disorders such as migraines, hearing and vision problems, Alzheimer's
CC disease, learning and memory disorders, seizures, psychotic disorders
CC and as neuroprotective agents e.g. to prevent stroke. Eag2 is useful
CC as a reporter molecule to measure changes in potassium concentration,
CC membrane potential, current flow, ion flux, transcription signal
CC transduction, receptor-ligand interactions, second messenger
CC concentration in vitro, in vivo and ex vivo, and also as indicator of
CC current flow in a particular direction. Detecting Eag2 nucleic acid
CC and protein expression is useful for diagnosing disease caused by
CC abnormal ion flux. Eag2 nucleotide and amino acid sequence information
CC may also be used to construct models of voltage-gated potassium channels
    in a computer system.
XX
SQ Sequence 2967 BP; 853 A; 663 C; 705 G; 746 T; 0 other;
```

```
Query Match 43.6%; Score 1294.4; DB 22; Length 2967;
Best Local Similarity 67.9%; Pred. No. 0;
Matches 1993; Conservative 0; Mismatches 811; Indels 132; Gaps 8;
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QY 7 atggtctgggggagagagagagtagtggccctcaaaaacagtttctgagaatattgt 66
    |||
Db 1 atgcgggggggagagagagagtagtggcccgagagacacattttggaacatcgtc 60
QY 67 cggcggtccaatgatactaatattgtgttggggaatgagtagtggagctgacctatt 126
    |||
Db 61 aggcgctccaggaatcaaatgattcttacttacttgggaattgccagattggtgtgcgtta 120
QY 127 gttacagcaatgatgatttgcagagctgtcgtgcctacacaggggagagagtgacaa 186
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Db 121 gttatagtaagagagaggttttgaacctctcgtgatataatcagagctgcgtcatgag 180
QY 187 aaaagcagacctgcagtttattatgtagtgggagctgactgataaagaacagatgaaaa 246
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QY 307 aacagagacacctgtgtgttcttctgtgaaatgtgcccaattgcaaacgagagataaa 366
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Db 301 aacagagacacccgtgtgttcttctgtgaaatgtgcccaattgcaaacgagagataaa 360
QY 367 gtgttttatttcttgcacttgcagtgacataacagcttcaaacagccaatttgagat 426
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Db 361 gtgtcttcttctcgtgtacttcaagatattagctgttcaaaagccaatttgagat 420
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QY 487 ggtgtcctgcagcagctgtgctccaagcgtgcgaaaaaggcgaagtgtcccaagcaactc 546
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QY 547 cgcctggcagaggttcctacagctgggctcagacatcctcccaagacaagagggca 606
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Db 538 agactagctggaagttctcagctgggatacgaatccctcctcagatataaacaagaagcg 597
QY 607 ccaagactccctcctacatacttcatattgtgttttaagaaccaagtggtgattgg 666
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Db 2794 gaaagcagtggtgacgaatttaataactctgtcggaataaagctaccaccagc 2849

RESULT 6

AAD04782

-ID AAD04782 standard; cDNA: 3289 BP.

XX AAD04782;

AC AAD04782;

DT 04-JUL-2001 (first entry)

XX

DE Human ether a gogo (hEAG2) cDNA.

XX

XX Human; ether a gogo; EAG2; cytosolic; neuroprotective; nootropic;

KW gene therapy; potassium ion channel; neurodegenerative disease; tumour;

KW Alzheimer's disease; Parkinson's disease; psoriasis; heart malfunction;

KW chromosome 14q22-24; cancer; cervix; breast; neuroblastoma; carcinoma;

KW congenital disease; arrhythmogenic right ventricular cardiomyopathy;

KW ARVC; lateral amyotrophic sclerosis; multiple sclerosis; ss.

XX

XX Homo sapiens.

XX

XX Key Location/Qualifiers

FT CDS 26..2992

FT /*tag= a

FT /product= "Human EAG2 (hEAG2)"

XX

XX MO200129068-A2.

XX

XX 26-APR-2001.

XX

XX 20-OCT-2000; 2000MO-EP10371.

XX

XX 20-OCT-1999; 99EP-0120784.

XX

XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX

XX Stuehmer W, Pardo L, Weseloh R;

XX

XX WPI: 2001-300317/31.

XX

XX P-PSDB: AAE01043.

XX

XX New nucleic acid encoding human K+ ion channel polypeptide for

PT prognosis of cancer, neurodegenerative diseases, including Alzheimer's,

PT Parkinson's disease, psoriasis and malfunction of heart -

XX

XX Claim 1; Fig 1; 62pp; English.

XX

XX The present is a cDNA encoding human potassium ion channel ether a gogo

CC (hEAG2) protein. The hEAG2 cDNA was obtained from human brain library.

CC The hEAG2 gene is located at position 22-24 of long arm of human

CC chromosome 14 (14q22-24). hEAG2 DNA and protein are useful for preventing

CC or treating a disease caused by undesired lack of expression, or

CC malfunction of hEAG2 protein. hEAG2 is also useful for preventing and/or

CC treating a congenital disease especially arrhythmogenic right ventricular

CC cardiomyopathy (ARVC); cancer including neuroblastoma, cervix carcinoma,

CC breast adenocarcinoma, breast carcinoma ductal type and/or

CC neurodegenerative diseases including Alzheimer's disease, Parkinson's

CC disease, lateral amyotrophic sclerosis or multiple sclerosis, psoriasis

CC and malfunction of heart and also for diagnosing tumours. hEAG2 DNA is

CC also useful in gene therapy.

XX

XX Sequence 3289 BP; 972 A; 708 C; 751 G; 858 T; 0 other;

XX

Query Match 43.6%; Score 1294.4; DB 22; Length 3289;

Best Local Similarity 67.9%; Pred. No. 0;

Matches 1993; Conservative 0; Mismatches 811; Indels 132; Gaps 8;

OY 7 atgagctgggagcaggaaggactagtcctcctcaaacagcttctgagagataatgtt 66

DB 26 atgcgcggggagcaagaagaggtgtgtgacccgcagacaacacatttttgaagaacatgc 85

OY 67 cggcggtcccaatgataactatttgtgttgggaatgctcaagatgaagtgactgctcatt 126

DB 86 aggcgcctccagatgaatcaagttcttacttctggaatgcccagatgttgatggcgtgta 145

OY 127 gtctacagcaatgattgttgaagctgtctgtgctatcaacagggaggaagtatgcaa 186

DB 146 gtttatagtaatacggtttttgttaaacctctctggaataatcatcagagctgacgtca 205

OY 187 aaaaagcagcacctgcaagtttatgtatggtggagctgacatgataaagaacagattgaaa 246

DB 206 aaaaagcagcaactgcaagtttatgtatggtggagctgacatgataaagaacagattgaaa 265

OY 247 gtgcgcgcaaacatttggaactatgagatgaatccttgaatcctgataagaagaag 306

DB 266 gtcaaggaacattttgcaactacgaaatcaaacagctcttgaagtcttctgttacaagaa 325

OY 307 aacagagcactctgtgttcttctgtgaaaatgtgccaacttcgaaaacgagcaagataa 366

DB 326 aacagagcctctgtgttcttctgtgaaaatgtgccaacttcgaaaatgaacatgaaaag 385

OY 367 gtgttatttcttctgcaacttctcaagtgacataaacagcttcaaacagccaattgagat 426

DB 386 gtgtctgttctctgttacttcaagatattacgttgttcaaacgccaattgagat 445

OY 427 gattcatgtaagagctgtggggaagttgtctgcgtcgaagaagcactgcaacagcagg 486

DB 446 gattcaacaaaagttgtgacgaaattgtcccgattgacacgggttcttgacaataagcga 505

OY 487 ggtgtcctgacagcagctggtcccaagcgtgcaaaaagcgagaatgtccacaagcattcc 546

DB 506 agtgttttgacagagctcagcgcaa---tgatataaacagaggtgtgtcctaataacatca 562

OY 547 cgcctgcaagagctccctacagctgtgctcaagacatccctcccaacgaagcagagca 606

DB 563 agactagctgaattctctcagcgtggtgacatataccttctcagatataacaagaagcg 622

OY 607 ccaagaactccctccacatcattacatattgtgttttaagaccagctggatgg 666

DB 623 ccaagagcgcacacacattatttactattgtgtcttttaaacactggtgattgg 682

OY 667 atcatcttgatcttgacctctctacagccatctgtgctccctataatgtcctcctaaa 726

DB 683 gtattttaaattcttccctctacacgcacatagttgttcttaaatgttccctcctaaa 742

OY 727 accagcagataatgtggtcgtgctgtgtgtatagacatcgtgagatattttgt 786

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OY 907 tgtttgcataatgataatcatcaacagcttcttgagaagctgagatgaggttagtgccttat 966

DB 923 tgtttacattatgacatcatcattgcttgaataatgtgagat----- 965

OY 967 ggtgattccaggaagattgtgttctgtatcagatctcaccacactgagggagagag 1026

DB 966 ----- 965

OY 1027 agtcaaggcatcagcagcctgttcaagctctcctaaagtttccggtcgtcgtctgtgg 1086

DB 966 ----aggaaatcagcagcgtctcctcctccttaaaagtgtgtcgtccttaagactgggc 1021

OY 1087 cgaatgtgcccgtgaagtgtgacacatacatgataatgagatcgtgtgctggtcgtgtg 1146

DB 1022 cgtgtgtgtgagaaactagcacttactagaaatattggaacagacagctccctgtgtcctgt 1081

OY 1147 gtgtgtgtgtgttggcgtggtcgtgacactgtgagcctgcatctgtatcagcattggggac 1206

Db 1082 gctgtgtgttctgactgtgcccactgtgctgtcatatgatatagcatcgagac 1141
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 Db 1142 tacgaggtcatgtatgaatgaatcaacacatcaatgaatgacaggtgtctaccgctg 1201
 Qy 1267 gcgatgtgacatttgcaccccttaccagtttaattggtctgtgtcgaaggaggtggaagt 1326
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 Db 1259 ggaaccagaagaattcatctgtatcgttctcctctacttaccatgacgaaccccttaca 1318
 Qy 1387 agtgtgtgtttggaacatcgcccatccacagacattgagaagattcttgcgtgtgc 1446
 Db 1319 accatagatgttggaaacatagctcctaccacagatgtgagaagaagtgttctgtgtgtc 1378
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 Qy 1507 caacgatgtatgtgcaaac 1566
 Db 1439 cagcaaatgtatgtccac 1498
 Qy 1567 cgaagccttaccaggtgtgcaaaagattgagtgagcgaatgaaatgtatgtgtgttc 1626
 Db 1499 cttaaaccttaccaggtgtgcaaaagccttgaagcgaatgaaatgtatgtgtgttc 1558
 Qy 1627 actgtgtcattgtccagagcattgtgacacagagaagtcctgtcagatctgtcccaagac 1686
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 Db 1619 atgagagcgtatctgt 1678
 Qy 1747 cgt 1806
 Db 1679 cgt 1738
 Qy 1807 gcccacagagac 1866
 Db 1739 gctcccgaggaccttaccatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1798
 Qy 1867 tctgtcctcctgt 1926
 Db 1799 tcaagatcctgt 1858
 Qy 1927 ggt 1986
 Db 1859 gtaattgt 1918
 Qy 1987 gcttgcactactgt 2046
 Db 1919 gcaactgacgtactgt 1978
 Qy 2047 tttctacagcgtccttctccatctcctcctcctcctcctcctcctcctcctcctcctcctcct 2106
 Db 1979 ttttatacagcgttcttgaac 2038
 Qy 2107 aagagagatgt 2166
 Db 2039 aacagagatcatcttctgt 2098
 Qy 2167 cgaagaatgt 2226
 Db 2099 cagaagaatgt 2158
 Qy 2227 agatltcgacagcagaagaaggt 2283

Db 2159 aagttcaagcagcagaagagctgtcggaatacaggtgtcaaacagaggtgtgacctgtgagag 2218
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 Qy 2244 ctgt 2403
 Db 2279 gt 2338
 Qy 2404 gcaagcctc-----cactcccggt 2456
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 Db 2459 ctgt 2518
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 Db 2699 gctgt 2758
 Qy 2782 gagggt 2841
 Db 2759 gaagtcaaac 2818
 Qy 2842 gagaac 2897
 Db 2819 gaaagcagcgt 2874
 RESULT 7
 AAC69494
 ID AAC69494 standard; cDNA; 1434 BP.
 XX
 AC AAC69494;
 DT 30-JAN-2001 (first entry)
 XX
 DE Human secreted protein gene 40 SEQ ID NO:50.
 XX
 KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
 KW antirheumatic; antiproliferative; cytosolic; carianth; vasotropic;
 KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
 KW fungicide; ophthalmologic; gene therapy; autoimmune disease; infection;
 KW hyperproliferative disorder; cardiovascular disorder; angiogenesis;
 KW cerebrovascular disorder; nervous system disorder; ocular disorder;
 KW wound healing; skin aging; food additive; preservative; ss.
 OS Homo sapiens.
 XX
 PN WO200058469-A1.
 XX
 PD 05-OCT-2000.
 XX
 PF 23-MAR-2000; 2000WO-US07579.
 XX

PR 26-MAR-1999: 99US-0126509.
PR 07-JAN-2000: 2000US-0174853.
XX
XX (HOMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Komatsoulis G;
XX
XX WPI: 2000-594642/56.
XX
XX P-PSDB: AAB38242.
PT Isolated nucleic acid molecule encoding a human secreted protein is
XX used in preventing, treating or ameliorating a medical condition
XX
XX Claim 1: Page 354-355; 416pp; English.
XX
XX The polynucleotide sequences given in AAC69455 to AAC69502 encode the
XX human secreted proteins given in AAB38203 to AAB38250. AAB38251 to
XX AAB38320 represent human secreted polypeptide sequences and proteins
XX homologous to them, which are given in the exemplification of the present
XX invention. Human secreted proteins have activities based on the tissues
XX and cells the genes are expressed in. Example of activities include:
XX immunosuppressive; antirheumatic; antineoplastic; antiproliferative;
XX cytostatic; cardiant; vasotropic; cerebroprotective; neurotropic;
XX neuroprotective; antibacterial; virucide; fungicide; and
XX ophthalmological. The polynucleotides and polypeptides can be used to
XX prevent, treat or ameliorate a medical condition in e.g. humans, mice,
XX rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
XX in diagnosing a pathological condition or susceptibility to a
XX pathological condition. Disorders which are diagnosed or treated include:
XX autoimmune diseases, hyperproliferative disorders, cardiovascular
XX disorders, cerebrovascular disorders, angiogenesis, nervous system
XX disorders, infections caused by bacteria, viruses and fungi and ocular
XX disorders. The polypeptides can also be used to aid wound healing and
XX epithelial cell proliferation, to prevent skin aging due to sunburn, to
XX maintain organs before transplantation, for supporting cell culture of
XX primary tissues, to regenerate tissues and in chemotaxis. The
XX polypeptides can also be used as a food additive or preservative to
XX increase or decrease storage capabilities. AAC69446 to AAC69454 and
XX AAB38202 represent sequences used in the exemplification of the present
XX invention.
XX
XX Sequence 1434 BP: 423 A; 256 C; 300 G; 452 T; 3 other:
SQ

Query Match 14.6%; Score 432.2; DB 21; Length 1434;
Best Local Similarity 99.5%; Pred. No. 4.7e-113;
Matches 431; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

00 1030 caggcgcacgacgacgtcttcagctctctaaagttgctcgcgctgctcgtctggcgca 1089
|||
79 caggcgcacgacgacgtcttcagctctctaaagttgctcgcgctgctcgtctggcgca 138
00 1090 gtggcgctgaagcttgaccacacattgaatgagctgctgctgctgctgctgctg 1149
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Db 139 gtggcgctgaagcttgaccacacattgaatgagctgctgctgctgctgctgctg 198
|||
00 1150 tgtgtgttggcgctgctgcacacgtgagctgctgctgctgctgctgctgctgctg 1209
|||
Db 199 tgtgtgttggcgctgctgcacacgtgagctgctgctgctgctgctgctgctgctg 258
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00 1210 gagatcttgcgagagac 1269
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Db 259 gagatcttgcgagagac 318
|||
00 1270 atggaacatggaccccttaccagtttaatgggtctgctcagggaagtgggaagtgtgt 1329
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Db 319 atggaacatggaccccttaccagtttaatgggtctgctcagggaagtgggaagtgtgt 378
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00 1330 ccagcgaagaattctgttaacatcccccgtgtgtatttcacacataccagcctaccagt 1389
|||
Db 379 ccagcgaagaattctgttaacatcccccgtgtgtatttcacacataccagcctaccagt 438
|||
00 1390 gtgggcttgggaacatgcgccatccacacacacacacacacacacacacacacacac 1449
|||

Db 439 gtgggcttgggaacatgcgccatccacacacacacacacacacacacacacacacac 498
|||
00 1450 atgatgatgctgt 1462
|||
Db 499 atgatgatgctgt 511
|||

RESULT 8
AAH21451
ID AAH21451 standard; DNA: 3479 BP.
XX
XX AAH21451:
XX
XX 18-SEP-2001 (first entry)
XX
XX Human HERG1 DNA.
XX
XX Inhibitor: eukaryotic; potassium channel; TRK1; TRK2; TOK1;
XX activator: ds.
XX
XX Homo sapiens.
XX
XX MO200151519-A2.
XX
XX 19-JUL-2001.
XX
XX 05-JAN-2001; 2001MO-EP00055.
XX
XX 11-JAN-2000; 2000DE-1000651.
XX
XX (AVENTIS PHARMA DEUT GMBH.
XX Leberer E, Leeuw T, Ritscher A;
XX
XX WPI: 2001-442137/47.
XX
XX Identifying inhibitors and activators of eukaryotic potassium channels,
XX for use as pharmaceuticals, comprises using yeast cells that express
XX heterologous, but no endogenous, potassium channels
XX
XX
XX Disclosure: Page 44-45; 78pp; German.
XX
XX This sequence represents a novel method for identifying inhibitors or
XX activators (A) of a eukaryotic potassium channel (KC) by applying a test
XX compound to a mutant *Saccharomyces cerevisiae* cell in which: (i) the
XX three endogenous KC (TRK1, TRK2 and TOK1) are not expressed; but (ii) a
XX eukaryotic KC is expressed heterologously, where the effect of the
XX compound on the eukaryotic KC is then determined. The method is used to
XX identify inhibitors or activators (A) of a eukaryotic potassium channel.
XX (A) are potentially useful as pharmaceuticals. The method is easily
XX automated for parallel processing of many samples, using either different
XX concentrations of test compounds and/or different levels of heterologous
XX gene expression. It allows identification of compounds that inhibit human
XX KC selectively. This sequence represents the human HERG1 encoding DNA
XX described in the method of the invention.
XX
XX Sequence 3479 BP: 604 A; 1237 C; 1055 G; 583 T; 0 other:
SQ

Query Match 11.4%; Score 339.2; DB 22; Length 3479;
Best Local Similarity 59.0%; Pred. No. 3.2e-86;
Matches 637; Conservative 0; Mismatches 413; Indels 30; Gaps 2;

00 1045 ctgttaagctcttaaaagtgtccggtctccgtctgtggcgagtgccggaagctg 1104
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Db 1558 ctgtagcggtcgtgaagactgcgcgctgctggtggtgcgctggcggaagctg 1617
|||
00 1105 gaccacttaacttaataatgagctgctgctgctgctgctgctgctgctgctgctg 1164
|||
Db 1618 gaccacttaacttaataatgagctgctgctgctgctgctgctgctgctgctgctg 1677
|||
00 1165 gtgcacacatgagctgctgctgctgctgctgctgctgctgctgctgctgctgctg 1224
|||

Db	1678	atcgcgcaatgctgtagctgcgacatctctgtacgctccatgcaacatgagcagccacacatg	1737
Qy	1225	gacacccaagaacatccgcgaacacacagctgtgtctcccaactagcgaatgagacattggaacc	1284
Db	1738	gactc-----acgcatacggctgtgcgcacaaacttgcgcacgaatagacaa	1785
Qy	1285	ccctacagatttaatggtctgtgcctcgaagggaatgtgggaagtgtgtccacgaagaattct	1344
Db	1786	ccctacacacagcagcggcctgggc-----ggccctcattcaagac	1827
Qy	1345	gtctacatccctccgtctgtatttccacaatgacacgacctaccagctgtggtcttggagac	1404
Db	1828	aagatattgacggcgctctacttccacttccacgacctccacagctccacagctgtggtcttgcgaac	1887
Qy	1405	atcgcccatccacagacacatttgaagaatctttgcgaatggtgcacatgatatgtatgtgtcca	1464
Db	1888	gtctctcccaacacacaaactcgaagaagatcttccatctgcatactgctatgctcatgtgtccc	1947
Qy	1465	ctctctcatgtccacatcttctcgggaattgtgagacactattttccacaacatgtatgccaac	1524
Db	1948	ctcatgtatgtctgacatctcttcgcgaacgctgtgcgcacatccatccacagcgtcttactcgggc	2007
Qy	1525	accacaacgatacccatgagatgctccacaacagctgtctcggagacttccctaagctccacaagctg	1584
Db	2008	acagcccgctacacacacacacacagatgcgcgggtgtgcgggaattatccgtcttccacacagtc	2067
Qy	1585	ccaaagagatttgaatgtagcgaatgatatgtatgttgcacttgttccatgttccatgttccaga	1644
Db	2068	cccaatccctcgtgcgaacgcgcttcgaggttacttccacagcacgctgtcttccacacac	2127
Qy	1645	ggcattgacacacagagaagtgtctctgcacatctgcgcccaagaaatgaaagacgcgaatctgc	1704
Db	2128	ggacatcgacacatgacgcgcgtgtgcgaaggcttccctctgaatgtccttgcacgcttgcacttgc	2187
Qy	1705	gtgcaccttgacacgcgaaggtgttccaaaggagacccggccttcccgcttgcgcagtgtatgc	1764
Db	2188	ctgcaccttgacacgcgttccactgtctgcacgactgtcaaaaccttccgaaggagccacaagagtc	2247
Qy	1765	tgacctccgggacacttggccatgtgagtttccacagctgtgcacagctgtgcacagggagacctatc	1824
Db	2248	tgcttcgggccttgcgcacatgaaatgttcaagacacacacatgacacgcgcagggagacacactgt	2307
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Qy	2065	catctcttcccggaacctgattctgcagctacacacttgaagaaagagatgtgtctccgg	2124
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Best Local Similarity 59.0%; Pred. No. 3.2e-86;
Matches 637; Conservative 0; Mismatches 413; Indels 30; Gaps 2;

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QY 1345 gtctacatctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1404
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Db 1948 ctcatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2007
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RESULT 10

AAA07602
ID AAA07602 standard; cDNA; 3950 BP.

AC AAA07602;

DT 19-JUN-2000 (first entry)

DE Long QT syndrome associated HERG protein encoding cDNA.

KW HERG; mutation; long QT syndrome; LQT syndrome; gene therapy; human; ss.

XX Homo sapiens.

OS WO200006772-A1.

PN 10-FEB-2000.

PD 20-JUL-1999; 99WO-US16337.

PR 27-JUL-1998; 98US-0122847.

PR 06-JAN-1999; 99US-0226012.

XX (UTAH) UNIV UTAH RES FOUND.

PI Keating MT, Splawski I;

XX WPI; 2000-195319/17.

DR P-PSDB; AAY85406.

PT New isolated mutant HERG nucleic acids, useful for developing products for the diagnosis, prevention and treatment of long QT syndrome -

XX Disclosure; Fig 8A-B; 163pp; English.

XX The invention relates to a HERG protein having a mutation compared to wild-type HERG, and is useful for developing products for the diagnosis, prevention and treatment of long QT (LQT) syndrome. The products and methods can be used for the diagnosis of subjects with LQT syndrome. They can also be used to screen for drugs for treating or preventing LQT syndrome. The HERG nucleic acids can also be used for gene therapy and CC HERG peptides can be used for peptide therapy. The present sequence represents the LQT syndrome associated HERG protein encoding cDNA.

XX Sequence 3950 BP; 695 A; 1369 C; 1210 G; 676 T; 0 other;

Query Match 11.4%; Score 339.2; DB 21; Length 3950;

Best Local Similarity 59.0%; Pred. No. 3.5e-86;
Matches 637; Conservative 0; Mismatches 413; Indels 30; Gaps 2;

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Db 1624 ctgctcgggtcgtcgaagactcgcgcgtcgtggtggtggtggtggtggtggtggtg 1683
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Db 1684 gatcgtactacagatgacgcgcgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1743
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OY	366	agtgtgttatcttcttcttgactcttcagcttgagcataag-----cttc	407
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DT	04-MAY-2000	(first entry)	
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XX			
KM	Voltage gated potassium channel subunit; VGPCs; heLK; human; stroke;		
KM	Kv superfamily; Bag family; ether a go-go; Elk subfamily; modulator;		
KM	chromosome 12q13; resting potential; cell excitability; seizure;		
KM	CNS; migraine; psychotic; anticonvulsant; ion flux disorder; detection;		
KM	gene therapy; antimigrane; cerebroprotective; neuroprotective;		
KM	antipsychotic; ss.		
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RESULT 2
US-09-226-012-3
Sequence 3, Application US/09226012
Patent NO. 6207383
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
TITLE OF INVENTION: SPILSKI, Igor
TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
FILE REFERENCE: 2323-136
CURRENT APPLICATION NUMBER: US/09/226,012
EARLIER APPLICATION NUMBER: 1999-01-06
EARLIER FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 3950
TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: CDS
LOCATION: (67) .. (3543)
US-09-226-012-3

Query Match 11.4%; Score 339.2; DB 4; Length 3950;
Best Local Similarity 59.0%; Pred. No. 4.1e-91;
Matches 637; Conservative 0; Mismatches 413; Indels 30; Gaps 2;

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Db      2554  ctacacaagatcatcatcgggagcagcctgcgtgaggtgctgcagacatgatacctccgagttccc 2613
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- Qy      2065  ccttccttcctcccggaacctgattctgacgtlacaacttgaggaagagatgtgtcccg 2124
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Db      2614  gaccactctcgtgcacagcctcgagatcacttcaactctgcgagataccacatgatcccg 2673

RESULT      3
US-08-956-242-3
/ Sequence 3, Application US/08956242C
/ Patent No. 5986081
/ GENERAL INFORMATION:
/ APPLICANT: Ganetzky, Barry S.
/ APPLICANT: Titus, Steven A.
/ TITLE OF INVENTION: Polynucleotides Encoding Herg-3
/ FILE REFERENCE: 960296.94550
/ CURRENT APPLICATION NUMBER: US/08/956,242C
/ NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 3
/ LENGTH: 3142
/ TYPE: DNA
/ ORGANISM: Homo sapien
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (34)..(2700)
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (3)
/ OTHER INFORMATION: Unidentified at time of filing
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (17)
/ OTHER INFORMATION: Unidentified at time of filing
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (31)..(32)
/ OTHER INFORMATION: Unidentified at time of filing
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (432)
/ OTHER INFORMATION: Unidentified at time of filing
/ FEATURE:
/ NAME/KEY: unsure
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/ OTHER INFORMATION: Unidentified at time of filing
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/ NAME/KEY: unsure
/ LOCATION: (1346)..(1348)
/ OTHER INFORMATION: Unidentified at time of filing
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1733)
/ OTHER INFORMATION: Unidentified at time of filing
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1737)
/ OTHER INFORMATION: Unidentified at time of filing
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1744)
/ OTHER INFORMATION: Unidentified at time of filing
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1746)

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OTHER INFORMATION:	Unidentified at time of filing
FEATURE:	
NAME/KEY: unsure	
LOCATION: (1758)	
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FEATURE:	
NAME/KEY: unsure	
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OTHER INFORMATION:	Unidentified at time of filing
FEATURE:	
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LOCATION: (1798)	
OTHER INFORMATION:	Unidentified at time of filing
FEATURE:	
NAME/KEY: unsure	
LOCATION: (1812)	
OTHER INFORMATION:	Unidentified at time of filing
FEATURE:	
NAME/KEY: unsure	
LOCATION: (1830)..(1831)	
OTHER INFORMATION:	Unidentified at time of filing
FEATURE:	
NAME/KEY: unsure	
LOCATION: (1855)	
OTHER INFORMATION:	Unidentified at time of filing
FEATURE:	
NAME/KEY: unsure	
LOCATION: (1862)	
OTHER INFORMATION:	Unidentified at time of filing
FEATURE:	
NAME/KEY: unsure	
LOCATION: (1864)	
OTHER INFORMATION:	Unidentified at time of filing
FEATURE:	
NAME/KEY: unsure	
LOCATION: (1895)	
OTHER INFORMATION:	Unidentified at time of filing
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LOCATION: (1900)	
OTHER INFORMATION:	Unidentified at time of filing
FEATURE:	
NAME/KEY: unsure	
LOCATION: (1903)	
OTHER INFORMATION:	Unidentified at time of filing
FEATURE:	
NAME/KEY: unsure	
LOCATION: (1915)..(1916)	
OTHER INFORMATION:	Unidentified at time of filing
FEATURE:	
NAME/KEY: unsure	
LOCATION: (1920)	
OTHER INFORMATION:	Unidentified at time of filing
FEATURE:	
NAME/KEY: unsure	
LOCATION: (1934)	
OTHER INFORMATION:	Unidentified at time of filing
FEATURE:	
NAME/KEY: unsure	
LOCATION: (1943)	
OTHER INFORMATION:	Unidentified at time of filing
FEATURE:	
NAME/KEY: unsure	
LOCATION: (1971)	
OTHER INFORMATION:	Unidentified at time of filing
FEATURE:	
NAME/KEY: unsure	
LOCATION: (1990)	
OTHER INFORMATION:	Unidentified at time of filing
FEATURE:	
NAME/KEY: unsure	
LOCATION: (2001)	
OTHER INFORMATION:	Unidentified at time of filing

1	FEATURE:	
2	NAME/KEY: unsure	
3	LOCATION: (1735)	
4	OTHER INFORMATION: Unidentified at time of filing	
5	FEATURE:	
6	NAME/KEY: unsure	
7	LOCATION: (1737)	
8	OTHER INFORMATION: Unidentified at time of filing	
9	FEATURE:	
10	NAME/KEY: unsure	
11	LOCATION: (1744)	
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13	FEATURE:	
14	NAME/KEY: unsure	
15	LOCATION: (1746)	
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17	FEATURE:	
18	NAME/KEY: unsure	
19	LOCATION: (1758)	
20	OTHER INFORMATION: Unidentified at time of filing	
21	FEATURE:	
22	NAME/KEY: unsure	
23	LOCATION: (1773)	
24	OTHER INFORMATION: Unidentified at time of filing	
25	FEATURE:	
26	NAME/KEY: unsure	
27	LOCATION: (1798)	
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29	FEATURE:	
30	NAME/KEY: unsure	
31	LOCATION: (1812)	
32	OTHER INFORMATION: Unidentified at time of filing	
33	FEATURE:	
34	NAME/KEY: unsure	
35	LOCATION: (1830) ..(1831)	
36	OTHER INFORMATION: Unidentified at time of filing	
37	FEATURE:	
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40	OTHER INFORMATION: Unidentified at time of filing	
41	FEATURE:	
42	NAME/KEY: unsure	
43	LOCATION: (1862)	
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46	NAME/KEY: unsure	
47	LOCATION: (1864)	
48	OTHER INFORMATION: Unidentified at time of filing	
49	FEATURE:	
50	NAME/KEY: unsure	
51	LOCATION: (1895)	
52	OTHER INFORMATION: Unidentified at time of filing	
53	FEATURE:	
54	NAME/KEY: unsure	
55	LOCATION: (1900)	
56	OTHER INFORMATION: Unidentified at time of filing	
57	FEATURE:	
58	NAME/KEY: unsure	
59	LOCATION: (1903)	
60	OTHER INFORMATION: Unidentified at time of filing	
61	FEATURE:	
62	NAME/KEY: unsure	
63	LOCATION: (1915) ..(1916)	
64	OTHER INFORMATION: Unidentified at time of filing	
65	FEATURE:	
66	NAME/KEY: unsure	
67	LOCATION: (1920)	
68	OTHER INFORMATION: Unidentified at time of filing	
69	FEATURE:	
70	NAME/KEY: unsure	
71	LOCATION: (1934)	
72	OTHER INFORMATION: Unidentified at time of filing	
73	FEATURE:	

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1 NAME/KEY: unsure
2 LOCATION: (1943)
3 OTHER INFORMATION: Unidentified at time of filing
4 FEATURE:
5 NAME/KEY: unsure
6 LOCATION: (1971)
7 OTHER INFORMATION: Unidentified at time of filing
8 FEATURE:
9 NAME/KEY: unsure
10 LOCATION: (1990)
11 OTHER INFORMATION: Unidentified at time of filing
12 FEATURE:
13 NAME/KEY: unsure
14 LOCATION: (2001)
15 OTHER INFORMATION: Unidentified at time of filing
16 FEATURE:
17 NAME/KEY: unsure
18 LOCATION: (2013)-(2019)
19 OTHER INFORMATION: Unidentified at time of filing
20 FEATURE:
21 NAME/KEY: unsure
22 LOCATION: (3124)
23 OTHER INFORMATION: Unidentified at time of filing
24 FEATURE:
25 NAME/KEY: unsure
26 LOCATION: (3135)
27 OTHER INFORMATION: Unidentified at time of filing
28 FEATURE:
29 NAME/KEY: unsure
30 LOCATION: (3141)
31 OTHER INFORMATION: Unidentified at time of filing
32 US-09-351-215-3

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Query Match	9.2%;	Score 272.8;	DB 3;	Length 3142;
Best Local Similarity	55.3%;	Pred. No. 2.8e-71;		
Matches 585;	Conservative 0;	Mismatches 446;	Indels 27;	Gaps 2

OY	1056	tccaaagttgtccggtgtgtccttcgttttgggcgaagtcgcccgaatgctggaaccataat	1115
Db	537	tttaagaaacttcgcgaactctcttcgtcttcttgccgctgmgcaggaaacttgcatactac	596
OY	1116	tgaatatgaaagctcctgtgtgtccgcgtcgtgtgtgtgtgttttgggcctgcgtacactg	1175
Db	557	agaaatagcgcgctgcgttcttaatgtctcaatgtcatalctttgtccctgaatgtcacctg	656
OY	1176	gatgcctgcacatcctgcgtacagcaatctggggactatgaatctcttgcagagaaaccaagac	1235
Db	657	gtcgtcttgctcttgcgtatgcgatttggaatgtgagaagccttaactg-----	705
OY	1236	aatccgcaacaacagcgtcgtctgtacaaactagcagatgacatgbcaccccttaccagt	1295
Db	706	-actgcacaatatcgatgtgttgcattccttaagacagacaatgtggaaacgtatacatga	764
OY	1296	taatgggtctggcttcaggggaagtcgggaagttgttcccaagaatctcgtttaatctc	1355
Db	765	cagtgactcaagttc-----ttgaccatcatcaataagacaataatcgttac	809
OY	1356	ctgtgttatcttcaatgacatgacagccctcacagtcacagttgggctttgggaatcgcccatc	1415
Db	810	agcccttaatttcaactcttcacgagtttaacagatgaaagatttcggaaatgcttccctaa	869
OY	1416	cacagacatttgagaagaaccttcttcagtcgbcacatgaaatgagatctgcactctctatgc	1475
Db	870	caggaattcggagaagaactctttcaatttggtcattgttgatgttgctcaactaatgtatgc	929
OY	1476	caccatcttcggaaatgtgacgaatactttccaacagatgatatgccaacacaacagata	1535
Db	930	aagcatctttgggatgtatctgcataattacccaagaagataactcggagatcgcagta	989
OY	1536	ccatgatgatgtcaacacagtttctgggaactctctgaaagctctacacagtcgccaagaagat	1595
Db	990	ccacatgcagatgctcgtgaataaagaatgttcatcttgccttccacaatctccacacctt	1049

Db 2016 acctgcggga 2025

RESULT 7

US-08-232-463-14/C
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: PTZgpt-Fls
; US-08-232-463-14

Query Match

Best Local Similarity 5.1%; Score 48.4; DB 1; Length 7218;
Matches 16; Conservative 177; Mismatches 123; Indels 0; Gaps 0;

Qy 2419 ggaggtgcagacacgaagctacagcgccaggtcagtgctcgagcccaagg 2478
Db 1352 RR 1293
Qy 2479 ggagggggcgatgtgcgaagcgcaaaagctggccgcttcaagatgtctggggaag 2528
Db 1292 RR 1233
Qy 2539 agtgaagcagcgaagcagtgctcaagcgctgaagtgtagacactccgaagaga 2598
Db 1232 RR 1173
Qy 2599 aaagcgtcagcagcgacacactgaagaagacagactcgtgtgacagtgcacccaag 2658
Db 1172 RR 1113

Qy 2659 agcgcattgcgctcygacaacgtgtgtgagggccaggaatcccaagatcggatccalc 2718
Db 1112 RR 1053
Qy 2719 ctggcagaggtcaagc 2734
Db 1052 CGACCTGCGAGCCAGC 1037

RESULT 8

US-08-046-585-15
; Sequence 15, Application US/08046585
; Patent No. 5453362
; GENERAL INFORMATION:
; APPLICANT: Lamarco, Kelly
; APPLICANT: Wilson, Angus
; APPLICANT: Herr, Winship
; TITLE OF INVENTION: A NOVEL EKARYOTIC TRANSCRIPTION PROTEIN:
; TITLE OF INVENTION: HOST CELL FACTOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/046,585
; FILING DATE: 12-APR-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-57503-1/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8252 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-046-585-15

Query Match

Best Local Similarity 48.6%; Score 43.4; DB 1; Length 8252;
Matches 115; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

Qy 2303 agggcaatgtcttcaagaagatgtcctcgcgaacacagcctcgtgaagcgaagcgtg 2362
Db 5530 AGAGCAATTGGCTCAATGATGCGCGGCGACGCTCCAGCACTGTGGCGTGCCTCCT 5589
Qy 2363 tcaecgtgtgagagtgctcgcacgcccgtatccttcaagcagcctccacctccggag 2422
Db 5590 CAACGGCCACGTGAGCGCTGCTCCATCCACACATTTGTGCCCCCGCGGCTTGTGG 5649
Qy 2423 tgcagaccacgaagatgaagcgccagggctcagtgctcgtggccccaaggaggggcg 2482
Db 5650 TGGCCAGCCAGCCAGCTGACGCTGACGCTACCTGACCGAAGTGGCAATGGCATCG 5709
Qy 2483 ggagcgattgtgcgaagcgaagcgtggcccgcttcaaaagtcttgcgggaagagt 2542

DB 5710 AGTCCCTGGGTGTGAAGCCAGACCTGCGCCGCCACCCAGCAGCAAGCCCATGAGAGG 5769
QY 2543 aggac 2547
DB 5770 AAAAC 5774

RESULT 9

US-08-393-703-15
Sequence 15, Application US/08393703
Patent No. 5585239
GENERAL INFORMATION:
APPLICANT: Lamarco, Kelly
APPLICANT: Wilson, Angus
APPLICANT: Herr, Winship
TITLE OF INVENTION: A NOVEL EKARYOTIC TRANSCRIPTION PROTEIN:
TITLE OF INVENTION: HOST CELL FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,703
FILING DATE: 24-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57503-2/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 8252 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PCT-393-703-15

Query Match 1.5%; Score 43.4; DB 1; Length 8252;
Best Local Similarity 48.6%; Pred. No. 0.035; Indels 0; Gaps 0;
Matches 119; Conservative 0; Mismatches 126;

QY 2303 agggcaatgtcttaccagagatgcttcgcaacacagccctcgtgaagcagcgctg 2362
DB 5530 AAGAGCAATGCTCATGAGCTGCGCGGACAGGTCCCGACACTGTGGCCTCTGCCCC 5589
QY 2363 tcaccgtgctgaagatctcgtccagcgcgtatctcttccagcagctccaccctcggg 2422
DB 5590 CAACGGCCACTGAGACCTGGCTCCATCCACACATTTGTGGCCCCCGACGCCGTTGTGG 5649
QY 2423 tgcacagcagcgaagctacagcgccaggtcgcagtgctcgtggccccaaggggggc 2482
DB 5650 TGGCGACGCCACGCAAGCTGACGGCTGCAGCTACCTGACCGAAGTGGCCCAATGCGATCG 5709
QY 2483 ggggagattgtgcgaagcgaagaagctggcccgcttcaaatgcttgcgggaagag 2542
DB 5710 AGTCCCTGGGTGTGAAGCCAGACCTGCGCCGCCACCCAGCAGCAAGCCCATGAGAGG 5769
QY 2543 aggac 2547

DB 5770 AAAAC 5774

RESULT 10

PCT-US93-11721-15
Sequence 15, Application PC/TUS9311721
GENERAL INFORMATION:
APPLICANT: Lamarco, Kelly
APPLICANT: Wilson, Angus
APPLICANT: Herr, Winship
TITLE OF INVENTION: A NOVEL EKARYOTIC TRANSCRIPTION PROTEIN:
TITLE OF INVENTION: HOST CELL FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11721
FILING DATE: 03-DEC-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: FP-57503-1/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 8252 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PCT-US93-11721-15

Query Match 1.5%; Score 43.4; DB 5; Length 8252;
Best Local Similarity 48.6%; Pred. No. 0.035; Indels 0; Gaps 0;
Matches 119; Conservative 0; Mismatches 126;

QY 2303 agggcaatgtcttaccagagatgcttcgcaacacagccctcgtgaagcagcgctg 2362
DB 5530 AAGAGCAATGCTCATGAGCTGCGCGGACAGGTCCCGACACTGTGGCCTCTGCCCC 5589
QY 2363 tcaccgtgctgaagatctcgtccagcgcgtatctcttccagcagctccaccctcggg 2422
DB 5590 CAACGGCCACTGAGACCTGGCTCCATCCACACATTTGTGGCCCCCGACGCCGTTGTGG 5649
QY 2423 tgcacagcagcgaagctacagcgccaggtcgcagtgctcgtggccccaaggggggc 2482
DB 5650 TGGCGACGCCACGCAAGCTGACGGCTGCAGCTACCTGACCGAAGTGGCCCAATGCGATCG 5709
QY 2483 ggggagattgtgcgaagcgaagaagctggcccgcttcaaatgcttgcgggaagag 2542
DB 5710 AGTCCCTGGGTGTGAAGCCAGACCTGCGCCGCCACCCAGCAGCAAGCCCATGAGAGG 5769
QY 2543 aggac 2547
DB 5770 AAAAC 5774

RESULT 11

US-07-708-038-3

Sequence 3, Application US/07708038

Patent No. 5268295

GENERAL INFORMATION:

APPLICANT: Sertero, Ginetie

TITLE OF INVENTION: MAMMALIAN ADIPOCYTE PROTEIN, NUCLEIC

TITLE OF INVENTION: ACIDS CODING

TITLE OF INVENTION: THEREFOR AND USES THEREOF

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Browdy and Neimark

STREET: 419 Seventh Street, NW

CITY: Washington

STATE: DC

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/708,038

FILING DATE: 19910531

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Livanat, Shmuel

REGISTRATION NUMBER: 33,949

REFERENCE/DOCKET NUMBER: SERPERO-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 444 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..444

US-07-708-038-3

Query Match

Best Local Similarity 1.4%; Score 40.2; DB 1; Length 444;

Matches 81; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

DB 2521 aaagatgctgcggaagagtgaggaacaggtgtccaaagctgagtgatgagag 2580

DB 208 AAAGATGCTGTGACGACTGTGACTGGGCGCAAGGATTTTGGCCAGCAGATCACA 267

QY 2581 acacttccgcagaggaagagcgtcagagccacactgaagaagacagactcgt 2640

DB 268 GGGGTGATGACAGACCAAGAGGGCGTGCAGTGTGAGAGACCAAGTCTGTG 327

QY 2641 gacagtgatccacacagagcagctgcg 2669

DB 328 GTCAGTGGCAGACATTACACAGCTTTGGG 356

RESULT 12

US-08-127-995-3

Sequence 3, Application US/08127995

Patent No. 5541068

GENERAL INFORMATION:

APPLICANT: Sertero, Ginetie

TITLE OF INVENTION: MAMMALIAN ADIPOCYTE PROTEIN, NUCLEIC

TITLE OF INVENTION: ACIDS CODING THEREFOR AND USES THEREOF

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Browdy and Neimark

STREET: 419 Seventh Street, NW

CITY: Washington

STATE: DC

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM compatible

STREET: 419 Seventh Street, NW

CITY: Washington

STATE: DC

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/127,995

FILING DATE: 15-NOV-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/708,038

FILING DATE: 31-MAY-1991

ATTORNEY/AGENT INFORMATION:

NAME: Townsend, G. Kevin

REGISTRATION NUMBER: 34,033

REFERENCE/DOCKET NUMBER: SERPERO-2A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 444 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..444

US-08-127-995-3

Query Match

Best Local Similarity 1.4%; Score 40.2; DB 1; Length 444;

Matches 81; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

DB 2521 aaagatgctgcggaagagtgaggaacaggtgtccaaagctgagtgatgagag 2580

DB 208 AAAGATGCTGTGACGACTGTGACTGGGCGCAAGGATTTTGGCCAGCAGATCACA 267

QY 2581 acacttccgcagaggaagagcgtcagagccacactgaagaagacagactcgt 2640

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DB 328 GTCAGTGGCAGACATTACACAGCTTTGGG 356

RESULT 13

US-08-764-343-2

Sequence 2, Application US/08764343

Patent No. 5739009

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Hawkins, Phillip R.

TITLE OF INVENTION: NOVEL ADIPOCYTE-SPECIFIC

TITLE OF INVENTION: DIFFERENTIATION-RELATED PROTEIN

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: US

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM compatible

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 9, 2001, 03:01:29 ; Search time 4156.91 Seconds
(without alignments)
11774.884 Million cell updates/sec

Title: US-09-694-777-14

Perfect score: 2967
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Scoring table:

IDENTITY_NUC
Gap 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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10	2368.2	79.8	3405	4	BTEAG1
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12	1310	44.2	3507	10	RN0250280
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ALIGNMENTS

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ACCESSION AX012972
VERSION AX012972.1 GI:10040220
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 2967)
Sanchez,P.A., Beckh,S., Stuehmer,W., Brueggemann,A., Pardo-Fernandez,L.A., Weseloh,R. and Del Camino Fernandez-Miranda,D.
Human k<-> ion channel and therapeutic applications thereof
Patent: WO 993463-A 14 28-OCT-1999;
MAX PLANC GESELLSCHAFT (DE); SANCHEZ PEREZ ARACELI (DE); BECKH SYNOEVE (DE); STUEHMER WALTER (DE); BRUEGEMANN ANDREA (DE); PARDO FERNANDEZ LUIS ANGEL (DE); WESELOH RUDIGER (DE); DEL CAMINO

TITLE JOURNAL
Human k<-> ion channel and therapeutic applications thereof
Patent: WO 993463-A 14 28-OCT-1999;
MAX PLANC GESELLSCHAFT (DE); SANCHEZ PEREZ ARACELI (DE); BECKH SYNOEVE (DE); STUEHMER WALTER (DE); BRUEGEMANN ANDREA (DE); PARDO FERNANDEZ LUIS ANGEL (DE); WESELOH RUDIGER (DE); DEL CAMINO

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DEFINITION	Sequence 2 from Patent WO954463.		
ACCESSION	AX012960		PAT 07-SEP-2000

VERSION	AX012960.1	GI:10040210
KEYWORDS		
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
AUTHORS	1 (bases 1 to 3083)	
TITLE	Sanchez, P.A., Beckh, S., Stuehmer, W., Brueggemann, A., Pardo-Fernandez, L.A., Weseloh, R. and Del Camilo Fernandez-Miranda, D.	
JOURNAL	Human k<+> ion channel and therapeutic applications thereof	
	Patent: WO 9554463-A 2 28-OCT-1999	
	MAX PLANCK GESELLSCHAFT (DE); SANCHEZ PEREZ ANACELI (DE); BECKH SYNOEVE (DE); STUEHMER WALTER (DE); BRUEGGMANN ANDREA (DE); PARDO FERNANDEZ LUIS ANGEL (DE); WESELOH RUEDIGER (DE); DEL CAMILO FERNANDEZ MIRANDA D (US)	
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Best Local Similarity	100.0%;	Pred. No. 0;
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RESULT 3
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DEFINITION Homo sapiens voltage-gated potassium channel eagb (EAG) mRNA,
complete cds.
ACCESSION AF078742
VERSION AF078742.1 GI:3790564
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3083)
Pardo, L.A., del Camino, D., Sanchez, A., Alves, F., Bruggemann, A.,
Beck, S. and Stuhmer, W.
Oncogenic potential of EAG K(+) channels
EMBO J. 18 (20), 5540-5547 (1999)
2 (bases 1 to 3083)
Pardo, L.A., del Camino, D., Sanchez, A., Beck, S. and Stuhmer, W.
Submitted (17-JUL-1998) MBNS, MPI exp. Medizin, Hermann-Rein-Str.
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AUTHORS	Sanchez, P.A., Beckh, S., Stuehmer, W., Brueggemann, A., Pardo-Fernandez, L.A., Weseloh, R. and Del Camino Fernandez-Miranda, D.		
TITLE	Human k<-> ion channel and therapeutic applications thereof		
JOURNAL	Patent: WO 9554463-A 13 28-OCT-1999.		

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Pardo, L.A., del Camino, D., Sanchez, A., Alves, F., Brugemann, A.,
Beckh, S. and Stuhmer, W.
Oncogenic potential of EAG K(+) channels
EMBO J. 18 (20), 5540-5547 (1999)
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JOURNAL 2 (bases 1 to 3002)
MEDLINE Pardo, L.A., del Camino, D., Sanchez, A., Beckh, S. and Stuhmer, W.
REFERENCE 1 (bases 1 to 3002)
AUTHORS Direct Submission
JOURNAL Submitted (17-JUN-1998) MBNS, MPI exp. Medizin, Hermann-Rein-Str.
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BASE COUNT 748 a 751 c 825 g 678 t
ORIGIN

Query Match 94.2%; Score 2795; DB 9; Length 3002;
Best local Similarity 97.3%; Pred. No. 0;

Matches 2886; Conservative 0; Mismatches 0; Indels 81; Gaps 1;
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Db 457 GAGGATGATTCATGTAAGAGCTGGGGGAAGTTGCTCGGCTACAAAGACACTGACAGC 516
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QY	2821	aacggcaaaatgaaccaatatttggaacaagcctctctagaatactcagaatataacttc	2880
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ACCESSION	AJ001366		
VERSION	AJ001366.1 GI:3676224		
KEYWORDS	potassium channel protein.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	1 (bases 1 to 3102)		
TITLE	Occhiodoro, T.		
JOURNAL	Direct Submission		
	Submitted (02-OCT-1997) Occhiodoro T., Department of Physiology, Centre Medical Universitaire, 1 Rue Michel Servet, Geneva 1211,		

REFERENCE	SWITZERLAND
2 (bases 1 to 3102)	
ATTNORS	Oochiodoro, T., Bernheim, L., Liu, J. H., Bijlenga, P., Simreich, M., Bader, C. R. and Fischer-Loughredo, J.
TITLE	Cloning of a human ether-a-go-go potassium channel expressed in myoblasts at the onset of fusion
JOURNAL	FEBS Lett. 434 (1-2), 177-182 (1998)
MDLINE	98408853
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Qy	841	attcttaccaccaactatccgactggaactaccctgaagacgtgtgtttgtatgtacctt	900
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Query Match	85.68;	Score 2538.6;	DB 4;	Length 3486;
Best Local Similarity	91.28;	Pred. No. 0;		
Matches 2707;	Conservative 0;	Mismatches 254;	Indels 6;	Gaps 1;
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Db	198	ATACCATGCTGGGGCAGAGAGGACCTGGTGGCCCGCAAAACAGCTTCTGGAGAAAT	257	
Db	61	attgttcgagcgtcccaatgaactaatttggcttggttggaatgctcagatagtgactg	120	
Db	258	ATTGTCGGGGGTCATGATGACTGTTGTTGGGGAATGCCAGATAGTGGACTGG	317	
Db	121	cctattgtgtaacagcaatgtatgttgcgaagctgtcgtgctatacagagcagaagt	180	
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DEFINITION Mus musculus potassium channel subunit (m-eag) mRNA, complete cds.
ACCESSION U04294
VERSION U04294.1 GI:487739
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 114 to 3083)
Warmeke, J.W. and Ganetzky, B.
A family of potassium channel genes related to eag in Drosophila and mammals
Proc. Natl. Acad. Sci. U.S.A. 91 (8), 3438-3442 (1994)
JOURNAL 94211879
MEDLINE 2 (bases 1 to 4010)
REFERENCE Warmeke, J.W.
AUTHORS Direct Submission
TITLE Submitted (10-DEC-1993) Jeffrey W. Warmeke, Genetics and Molecular Biology, Merck Research Laboratories, 126 East Lincoln Avenue, P.O. Box 2000, Rahway, NJ 07065, USA
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 Saganah,M.J., Vega-Saenz de Miera,E., Nadal,M.S., Baker,H.,
 Coetzee,W.A. and Rudy,B.
 Cloning of components of a novel subthreshold-activating K(+) channel with a unique pattern of expression in the cerebral cortex
 J. Neurosci. 19 (24), 10789-10802 (1999)
 MEDLINE 20063035
 JOURNAL
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 Saganah,M.J., Vega-Saenz de Miera,E., Nadal,M.S., Baker,H.,
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 University School of Medicine, 550 First Avenue, New York, NY
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Chemistry: Dye-terminator Big Dye; 100% of reads
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

201 nucleic - nucleic search, using sw model

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(without alignments)
13009.959 Million cell updates/sec

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 537289281 residues

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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18	177.8	6.0	281	11 F05456	F05456 HSC08F091 n
19	176.4	5.9	791	10 AU080193	AU080193 AU080193
20	168.8	5.7	760	13 CNS0343V	AL243796 Tetradon
21	164	5.5	850	13 CNS03MKD	AL263830 Tetradon
22	161	5.4	1063	13 CNS0422O	AL270969 Tetradon
23	160	5.4	803	10 BE382810	BE382810 601297818
24	159.4	5.4	926	11 BF315250	BF315250 601899133
25	158.2	5.3	1048	13 CNS02B82	AL190165 Tetradon
26	156.6	5.3	884	11 BF311665	BF311665 601897141
27	156.6	5.3	1101	13 CNS05AWH	AL329066 Tetradon
28	156.2	5.3	769	13 CNS04KEY	AL294739 Tetradon
29	155.2	5.2	365	10 BB314638	BB314638 BB314638
30	153	5.2	816	13 CNS02X0V	AL217768 Tetradon
31	150.6	5.1	282	10 BB315188	BB315188 BB315188
32	150.4	5.1	501	11 B1341020	B1341020 368212 MA
33	150.2	5.1	914	13 CNS03WKE	AL263831 Tetradon
34	146.2	4.9	240	10 BB312893	BB312893 BB312893
35	145.8	4.9	853	13 CNS03QSO	AL263533 Tetradon
36	144.4	4.9	1013	13 CNS0511Y	AL316303 Tetradon
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38	138	4.7	1036	13 CNS0020R	AL061908 Drosophila
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40	136.8	4.6	501	10 AW249298	AW249298 2821074.5
41	134	4.5	716	13 CNS04ABX	AL281562 Tetradon
42	132.8	4.5	1084	13 CNS057J2	AL334695 Tetradon
43	131.2	4.4	840	11 R55596	R55596 y988f08.r1
44	129.8	4.4	893	11 BF317069	BF317069 601903465
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ALIGNMENTS

RESULT 1
LOCUS U69185 1706 bp mRNA EST 27-OCT-1999
DEFINITION U69185 Soares infant brain INIB Homo sapiens CDNA clone c-b0f09,
U69185
ACCESSION U69185.1 GI:2739409
VERSION
KEYWORDS
SOURCE EST.
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1706)
Volorio, S., Simon, G., Repetto, M., Cucchiardi, M., Banfi, S., Borsani
G., Ballabio, A. and Zollo, M.
Sequencing analysis of forty-eight human image cDNA clones similar
to drosophila mutant protein
DNA Seq. 9 (5-6), 307-315 (1998)
JOURNAL
MEDLINE 99452388
COMMENT Contact: Zollo, Massimo
Telethon Institute of Genetics and Medicine
Via Olgettina 58, Milan, MI 20132, Italy
Email: zollo@tigem.it.
FEATURES
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[illegible][illegible]


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            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
            1 (bases 1 to 945)
REFERENCE   Roest-Crollius, H., Jaillon, O., Dasilva, C., Fitzames, C., Fisher, C.,
AUTHORS     Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
            Weissenbach, J.
TITLE       Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 945)
AUTHORS     Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
            Bernot, A., Fitzames, C., Wincker, P., Brothier, P., Quetier, F.,
            Saurin, W. and Weissenbach, J.
TITLE       Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
JOURNAL     Unpublished
REFERENCE   3 (bases 1 to 945)
AUTHORS     Genoscope.
TITLE       Direct Submission
COMMENT     Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
            This sequence is a single read and was generated as part of a large
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            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
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Matches 508; Conservative 2; Mismatches 142; Indels 146; Gaps 2;
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QY 1643 gaaggatgacacagaga----- 1660
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Db 536 AGCGACGGCTGCTGCGCTCTCTGCGCTGAGCTTCACAGCACATCTAGCCGCCCGCCG 477
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Db 476 GACATCATCTTCCACCTCGCGGAGAGACGTGAGAACCCCTGCTTCTGCTGGGCTCC 417
QY 1876 ctgagagtgatcacaagatgatgagtgagtgagcattct----- 1913
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QY 1914 -----agg 1916
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QY 1917 aaagagagacgttttgagatgtgtctggaagagacaccccttcagcctgtgac 1976
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
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        UI-M-BH3-bsh-d-08-0-UI.s1 NIH_BMAP_M.S4 Mus musculus cDNA clone
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    ACCESSION
        B1134074
    VERSION
        B1134074.1 GI:14584322
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        house mouse.
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        Mus musculus.
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
    REFERENCE
        1 (bases 1 to 557)
        Bonaldo, M.F., Lennon, G. and Soares, M.B.
        Normalization and subtraction: two approaches to facilitate gene
        discovery
        Genome Res. 6 (9), 791-806 (1996)
    JOURNAL
        MEDLINE
        97044477
        Contact: Chin, H
        National Institute of Mental Health
        6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
        20892-9643, USA
        Tel: 301 443 1706
        Fax: 301 443 9890
        Email: MEST@mail.nih.gov
        Oligo-dT track not found. Not 1 site shown in beginning of sequence
        is likely internal to the message. cDNA library preparation: M.B.
        Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
        clones from RESEARCH GENERAL. It should be noted that Bento Soares
        is generating a small number of additional specialized
        non-redundant arrays of BMAP cDNAs whose availability will be
        considered under appropriate and limited collaborative arrangements
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        POLYA-NO.
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TAG_SEQ=None found"

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/note="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_M_S4 library is a subtracted library of a series
ultimately derived from a mixture of individually tagged
normalized libraries from ten regions of the mouse brain
(cerebellum, brain stems, olfactory bulbs, hypothalamus,
cortex, amygdala, basal ganglia, pineal gland, striatum,
hippocampus) after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries
were generated in this process: NIH_BMAP_M_S4,
NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1,
NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library
(NIH_BMAP_M_S4) was constructed as follows: PCRamplified
cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and
NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived
was used as a driver in a hybridization with a pool of
the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1
libraries in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library)
was purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
NIH_BMAP_M_S4 library. This procedure has been previously
described (Bonaldi, Lennon and Soares, Genome Research
6:791-806, 1996)

Query Match	6.8%	Score 202.2	DB 11	Length 557
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QY 1446	catcatgtgatgttgctcaactctctatagccacatcttcgggaatgtggaactattt	1505		
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QY 1566	ccatgaagctctaccagatgtgcacaaagaattgagtgcagtgtaatgatatattgtgc	1625		
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QY 1626	caattgtgcattgtccgaagcatltgaaacacagagaaggttcctgcagacatctgcgccaaaga	1685		
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QY 1686	catgagagccacacatctgctgcacatctaaacccgaagtglttcaagagacccggctt	1745		
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Db 197	CCGAGGCGCCACTAAAGGCTCGCTGAGGCGCGCTGCTGTGAAGTTCAAGACACACATGCG	138		
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QY 1866	tctctgtccctctgaggtgatccaaagatgtaggtgtgctgacatcttcaagaaagaga	1925		
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REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
COMMENT			
FEATURES			
SOURCE			
BASE COUNT			
ORIGIN			
Query Match			
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61	gtttttaaTGAACATNCtGCTTTCGATTGGCCAGCGATGGGTGTCtCCNGCCCTTGGCG	120	
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121	GTAGAGTTCCAACACATTCtACTGTCTCTCCGGGAGACCTCATTTTACCATGCGGAGAAAGT	180	
1843	gttcagacgtctgtgcttgcgttctgcgtccctctgagagtgatccaaagatgatgaagtg	1902	

Db 181 GTGACATGCCCTCTGCTTGTGTGGTGTGCAGACATCCCTTGGAAAGTCATCAGACATGATGAGG 240
Oy 1903 gtggccattctcaggaagaagagagctgtcttggagatgtcttcctggaaagagcaacctt 1962
Db 241 GTGGCTATTATTGAAGGAAGGATGATGATTATTGGAGACATCTTCTGGAGAAACACACCTT 300
Oy 1963 gccca 1967
Db 301 GCCCA 305

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BB315626
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DEFINITION
KEYWORDS
ACCESSION
VERSION
KEYWORDS
ORGANISM
SOURCE
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BB315626 372 bp mRNA EST 11-JUL-2000
BB315626 RIKEN full-length enriched, adult male corpora
quadrigenina Mus musculus cDNA clone B230359A06 3' similar to
004294 Mus musculus potassium channel subunit (m-eag) mRNA, mRNA
sequence.
BB315626
BB315626.1 GI:9022661
EST.
Mus mouse.
house mouse.
house mouse.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 372)
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci,
P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hizano, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata,
Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,
Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya,
T., Tsunoda, Y., Watabiki, A., Watanabe, S., Yamamura, T., Yamanaka, I.,
Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino,
M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Konno, H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki,
N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermosensitization and thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Katsunari, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

location/Qualifiers
1..372
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FEATURES
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		PLC I."
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ORIGIN		
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Best Local Similarity	78.2%: Pred. No. 2.1e-41;	
Matches 262:	Conservative 0; Mismatches 71; Indels 2; Gaps 2;	
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Qy	2693 ggagttcccaagatcgaagtcctccactcctcygcaaggatcaagcatcgttclaccattcc 2752	
	74 GGAGTCCTCAGGA-CCGACCCTTATCTTGCCCGAGGTCACAGCATTTCTTACCCCATCC 132	
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	193 AGCCTTGAATGCCAAATGACCTTCATTTGGAAGAACACTTTTGTAGTACTCAGATTAC 252	
Qy	2873 taacttcagaagaatcctctcagtcctcctcagtgagtglttgaatatcgaagccacagt 2932	
	253 TAATGTCCAGAGAGGTCCTCCCAATCTCTTCAGGAGACGGGTGAGATCTCCAGCCCCCATY 312	
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	313 CCCCAGAGTCAGACAGACATTTTTGGACCAAGC 347	
RESULT 11		
LOCUS	BB317367	
DEFINITION	BB317367 RIKEN full-length enriched, adult male corpora quadrigenina Mus musculus cDNA clone B230369B1 3' similar to U04294 Mus musculus potassium channel subunit (m-eag) mRNA, mRNA sequence.	
ACCESSION	BB317367	
VERSION	BB317367.1 GI:9024402	
KEYWORDS	EST.	
SOURCE	Mus musculus.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 315)	
AUTHORS	Kono,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hoti,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,K., Kiluchi,N., Kiyaosawa,H., KoJima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.	

Matsuyma,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.
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